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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:21 ; Search time 1381.16 Seconds
(without alignments)
22.376 Million cell updates/sec

Title: US-09-709-170A-17
Sequence: 1 tctccagcgtcgcacat 18
Scoring table: GAPOP 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AA086659	Bcl-2 antisense ol
2	18	100.0	18	AAV52545	Unmethylated Cpg d
3	18	100.0	18	AAV27719	Immunostimulatory
4	18	100.0	18	AAV28181	Antisense oligonuc
5	18	100.0	18	AAV19667	Human bcl-2 antise
6	18	100.0	18	AAZ31944	Cpg adjuvant oligo
7	18	100.0	18	AAZ41905	IL-12 secretion in
8	18	100.0	18	AAZ41948	IL-12 secretion in
9	18	100.0	18	AAV8803	HPV fusion protein

10	18	100.0	18	AAV88537	Cytosine-guanosine
11	18	100.0	18	AAV33514	Bcl2-targeted anti
12	18	100.0	18	AAV23893	Deletion sequence
13	18	100.0	18	AAV27536	Synthetic RNA sequ
14	18	100.0	18	AAV18702	Target bcl-2 anti
15	18	100.0	18	AAV94434	Antisense oligonuc
16	18	100.0	18	AAV64137	Immunostimulatory
17	18	100.0	18	AAV60237	Immunostimulatory
18	18	100.0	18	AAV65037	Bcl2 antisense seq
19	18	100.0	18	AAV90450	Cpg adjuvant oligo
20	18	100.0	18	AAV91620	Human Bcl-2 antise
21	18	100.0	18	AAV9264	Cpg immunostimulat
22	18	100.0	18	AAV14470	Phosphorothioate o
23	18	100.0	18	AAV38517	Oligonucleotide us
24	18	100.0	18	AAV29003	Cpg motif for immu
25	18	100.0	18	AAV60975	Nucleotide sequenc
26	18	100.0	18	AAV27997	BRE-labeled oligo
27	18	100.0	18	AAV29860	Human Bcl-2 therap
28	18	100.0	18	AAV27643	Parasitic infectio
29	18	100.0	18	AAV24780	Immunostimulatory
30	18	100.0	18	AAV247850	Immune remodeling
31	18	100.0	18	AAV247981	Immune remodeling
32	18	100.0	18	AAV248024	Cpg-containing oli
33	18	100.0	18	AAV50615	Natural killer cel
34	18	100.0	18	AAV20395	Cpg motif containi
35	18	100.0	18	AAV98832	Cpg immunostimulat
36	18	100.0	18	AAV98885	Immunostimulatory
37	18	100.0	18	AAV98929	Immunostimulatory
38	18	100.0	18	AAV98930	Immunostimulatory
39	18	100.0	18	AAV98966	Immunostimulatory
40	18	100.0	18	AAV60923	Anti-bcl oligonuc
41	18	100.0	18	AAV59502	Immunostimulatory
42	18	100.0	18	AAV27748	P. falciparum vacc
43	18	100.0	18	AAV27362	Cg motif and CPA c
44	18	100.0	18	AAV19305	Cpg oligonucleotid

ALIGNMENTS

RESULT	ID	AA086659 standard; DNA; 18 BP.	Location/Qualifiers
1	AA086659	27-SEP-1995 (first entry)	1..18
XX	AC	AA086659;	/*tag= a
XX	AC	Bcl-2 antisense oligonucleotide.	/note= "3'-5' (antisense) sequence"
XX	DE	Bcl-2 antisense oligonucleotide.	
XX	DE	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy.	
XX	KW	Chemoresistance; ss.	
XX	KW	Synthetic.	
XX	OS	Key	
XX	FT	Misc_Feature	
XX	FT	Location/Qualifiers	
XX	FT	1..18	
XX	FT	/*tag= a	
XX	FT	/note= "3'-5' (antisense) sequence"	
XX	PN	W0508350-A.	
XX	PD	30-MAR-1995.	
XX	PD	20-SEP-1994;	94WO-US10725.
XX	PF	20-SEP-1993;	93US-0124256.
XX	PR	(REED/) REED J C.	
XX	PA	Read JC;	
XX	PI		
XX	XX		

DR WPI: 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer

XX Example 18; Page 44; 108pp; English.

XX Reversal of chemoresistance of tumor cells by antisense-mediated
CC reduction of bcl-2 expression was demonstrated using the
CC oligonucleotide given in AAO86659. This is antisense to the first
CC 6 codons of the bcl-2 ORF.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

XX Query Match

Best Local Similarity 100.0%; Score 18; DB 16; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccacagctgcgccat 18
Db 1 tctccacagctgcgccat 18

RESULT 2

AAV52545
ID AAV52545 standard; DNA; 18 BP.

XX AAV52545;

XX 20-NOV-1998 (first entry)

XX Unmethylated Cpg dinucleotide 1758.

XX Unmethylated Cpg dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.

XX Synthetic.

XX WO9837919-A1.

XX 03-SEP-1998.

XX 25-FEB-1998; 98WO-US03678.

XX 28-FEB-1997; 97US-0039405.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Schwartz DA;

XX WPI: 1998-480941/41.

XX Use of nucleic acids containing an unmethylated Cpg - for treating a
PT subject having or at risk of having an acute decrement in air flow
PT or inhibiting an inflammatory response

XX Example 4; Page 35; 65pp; English.

XX This sequence represents an unmethylated Cpg dinucleotide, and can be
CC having, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated Cpg. The nucleic acid sequence containing at least one
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with

CC Gram-positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, gram-negative pneumonia, gram-negative abdominal
CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide.

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

XX Query Match

Best Local Similarity 100.0%; Score 18; DB 19; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccacagctgcgccat 18
Db 1 tctccacagctgcgccat 18

RESULT 3

AAV27719
ID AAV27719 standard; DNA; 18 BP.

XX AAV27719;

XX 01-OCT-1998 (first entry)

XX Immunostimulatory oligodeoxyribonucleotide of the invention.

XX Immunostimulatory; oligodeoxyribonucleotide; ODN.

XX unmethylated Cpg dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.

XX Synthetic.

XX WO9818810-A1.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-US19791.

XX 30-OCT-1996; 96US-0738652.

XX (IOWA) UNIV IOWA RES FOUND.

XX Kline JN, Krieg AM;

XX WPI: 1998-272127/24.

XX New immunostimulatory nucleic acid molecules - which contain at
PT least one unmethylated Cpg dinucleotide, used for treating e.g.
PT tumours, infections or autoimmune disease

XX Disclosure; Page 49; 109pp; English.

XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides
CC (ODNs) of the invention. The ODNs contain at least one unmethylated Cpg
CC dinucleotide, and have the formula:
CC 5' N1X1G4X2N2 3', where at least one nucleotide separates consecutive
CC Cpgs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N
CC is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and
CC OR 5' N1X1G4X2N2 3', where at least one nucleotide separates
CC consecutive Cpgs, X1 and X2 are selected from GPT, GCG, GGA, APT and APA,
CC X3 and X4 are selected from TPT or CPT, N is any nucleotide and N1+N2 is
CC 0-26 bases with the provision that N1 and N2 does not contain a CCGG
CC tetramer or more than one CCG or CCG trimer.

CC The ODNs activate lymphocytes in a subject and redirect a subject's
CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells
CC and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune diseases, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a

CC human.
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 4

AAV28181
 ID AAV28181 standard; DNA; 18 BP.

XX AAV28181;
 AC

DT 08-OCT-1998 (first entry)
 XX

DE Antisense oligonucleotide to bcl-2 mRNA.
 XX

KW Purification: oligonucleotide; matrix; affinity unit;
 affinity purification; antisense; bcl-2; ss.
 XX

OS Synthetic.
 XX

PN WO9827425-A1.
 XX

PD 25-JUN-1998.
 XX

PF 18-DEC-1997; 97WO-US23284.
 XX

PR 19-DEC-1996; 96US-0769951.
 XX

PA (ISIS-) ISIS PHARM INC.
 XX

PI Chen D, Cole DL, Srivatsa GS;
 XX

DR WPI; 1998-362922/31.
 XX

PT Matrix for selective separation of oligo:nucleotide - useful for,
 e.g. large scale purification of anti-sense agents from their
 XX

PT deletion derivatives formed during synthesis
 XX

PS Disclosure; Page 86; 18pp; English.
 XX

XX AAV28181-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridising portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.
 CC

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 5

AAV19667
 ID AAV19667 standard; DNA; 18 BP.

XX AAV19667;
 AC

DT 12-JUN-1998 (first entry)
 XX

DE Human bcl-2 antisense oligonucleotide 13.
 XX

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 cancer; ss.
 XX

OS Synthetic.
 XX

OS Homo sapiens.
 XX

PN US5734033-A.
 XX

PD 31-MAR-1998.
 XX

PF 24-MAR-1994; 94US-0288692.
 XX

PR 21-FEB-1992; 92US-0840716.
 XX

PR 22-DEC-1988; 88US-0288692.
 XX

PR 24-MAR-1994; 94US-0217082.
 XX

PA (TYPE-) UNIV PENNSYLVANIA.
 XX

PI Reed J;
 XX

DR WPI; 1998-229881/20.
 XX

PT Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX

PS Disclosure; Column 23; 21pp; English.
 XX

XX This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of
 CC a functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 CC

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 6

AAZ31944
 ID AAZ31944 standard; DNA; 18 BP.

XX AAZ31944;
 AC

DT 26-JAN-2000 (first entry)
 XX

DE Cpg adjuvant oligo 1002.
 XX

KW Cpg adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
 antigen; infection; allergy; cancer; therapy; ss.
 XX

OS Synthetic.
 XX

XX PN W09952549-A1.
 XX PD 21-OCT-1999.
 XX PF 29-MAR-1999; 99WO-EP02278.
 XX PR 09-APR-1998; 98GB-0007805.
 XX PR 25-SEP-1998; 98GB-0020956.
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX PI Friede M, Hermand P;
 XX DR WPI; 1999-620290/53.
 XX PT Vaccine to protect against infections, allergy and cancer -
 XX PS Example 9; Page 26; 52pp; English.
 CC This sequence represents a CpG adjuvant that can be used in the vaccine
 CC composition of the invention. The vaccine comprises a polyoxyethylene
 CC ether or ester (I), not in the form of a vesicle, pharmaceutically
 CC acceptable excipient and an antigen (Ag) or antigenic composition. The
 CC vaccine can be used to treat or prevent infections (by bacteria, viruses
 CC or other parasites), allergy and cancer. (I), which are safe, easy to
 CC sterilize and simple to administer, are powerful vaccine adjuvants, able
 CC to induce a systemic immune response when administered (non-invasively)
 CC to the mucosa. The response is at least as good as that from conventional
 CC reactogenicity and are well tolerated.
 XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 20; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 Db 1 tctccagcgtgcgcacat 18

RESULT 7
 AAZ41905
 ID AAZ41905 standard; DNA; 18 BP.
 XX AC AAZ41905;
 XX DT 24-JAN-2000 (first entry)
 XX DE IL-12 secretion inducing CpG oligonucleotide 50.
 XX KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
 XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 XX KW antigen presenting cell; infection; allergic disease.
 XX OS Synthetic.
 XX PN W09951259-A2.
 XX PD 14-OCT-1999.
 XX PF 02-APR-1999; 99WO-US07335.
 XX PR 03-APR-1998; 98US-0080729.
 XX PA (IOWA) UNIV IOWA RES FOUND.
 XX PI Krieg AM, Weiner G;
 XX

DR WPI; 1999-620169/53.
 XX Novel synergistic combinations of immunostimulatory oligonucleotides
 XX and immunopotentiating cytokines are useful for stimulating the immune
 XX system -
 XX PS Example 8; Page 80; 91pp; English.
 CC Sequences AAZ41856-241949 are phosphorothioate CpG oligonucleotides
 CC which are used in the invention to induce interleukin-12 (IL-12)
 CC secretion from human PBMC. The invention comprises stimulating an immune
 CC response in a subject comprising administering to a subject exposed to an
 CC antigen, an immunopotentiating cytokine and an immunostimulatory CpG
 CC oligonucleotide to induce a synergistic and an immunostimulatory CpG
 CC response. The methods are useful for treating cancer by stimulating an
 CC antigen specific immune response against a cancer antigen. The methods
 CC can also be used to treat neoplastic disorders in humans, including but
 CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
 CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
 CC for treating infectious diseases, e.g. viral diseases such as HIV,
 CC bacterial diseases, and fungal diseases. The methods may also be used to
 CC treat allergic diseases, e.g. asthma. The methods and compositions may
 CC also be applied to treat cancer and tumors in non human subjects,
 CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
 CC be treated and include leukaemia, haemangioepithelioma and bovine ocular
 CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
 CC caused by the bacterium Corynebacterium pseudotuberculosis, and
 CC treated. CpG oligonucleotides can be useful in activating B cells, NK
 CC cells, and antigen presenting cells, such as monocytes and macrophages.
 CC CpG oligonucleotides enhance antibody dependent cellular cytotoxicity and
 CC can be used as an adjuvant in conjunction with tumour antigens to
 CC protect against a tumour challenge.
 XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 20; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 Db 1 tctccagcgtgcgcacat 18

RESULT 8
 AAZ41948
 ID AAZ41948 standard; DNA; 18 BP.
 XX AC AAZ41948;
 XX DT 24-JAN-2000 (first entry)
 XX DE IL-12 secretion inducing CpG oligonucleotide 93.
 XX KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
 XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 XX KW antigen presenting cell; infection; allergic disease.
 XX OS Synthetic.
 XX PN W09951259-A2.
 XX PD 14-OCT-1999.
 XX PF 02-APR-1999; 99WO-US07335.
 XX PR 03-APR-1998; 98US-0080729.
 XX PA (IOWA) UNIV IOWA RES FOUND.
 XX

PI Krieg AM, Weiner G;
XX
XX WPI: 1999-620169/53.
PT Novel synergistic combinations of immunostimulatory oligonucleotides
PT and immunopotentiating cytokines are useful for stimulating the immune
PT system -
XX
XX Example 8; Page 88; 91pp; English.
PS
XX Sequences AA241856-241949 are phosphorothioate Cpg oligonucleotides
CC which are used in the invention to induce interleukin-12 (IL-12)
CC secretion from human PBMC. The invention comprises stimulating an immune
CC response in a subject comprising administering to a subject exposed to an
CC antigen, an immunopotentiating cytokine and an immunostimulatory Cpg
CC oligonucleotide to induce a synergistic antigen specific immune
CC response. The methods are useful for treating cancer by stimulating an
CC antigen specific immune response against a cancer antigen. The methods
CC can also be used to treat neoplastic disorders in humans, including but
CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC for treating infectious diseases, e.g. viral diseases such as HIV,
CC bacterial diseases, and fungal diseases. The methods may also be used to
CC treat allergic diseases, e.g. asthma. The methods and compositions may
CC also be applied to treat cancer and tumours in non human subjects, may
CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC be treated and include leukaemia, haemangioendothelioma and bovine ocular
CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC caused by the bacterium *Corynebacterium pseudotuberculosis*, and
CC contagious lung tumour of sheep caused by *Jaagsiekte* may also be
CC treated. Cpg oligonucleotides can be useful in activating B cells, NK
CC cells, and antigen presenting cells, such as monocytes and macrophages.
CC Cpg oligonucleotides enhance antibody dependent cellular cytotoxicity and
CC can be used as an adjuvant in conjunction with tumour antigens to
CC protect against a tumour challenge.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgccat 18
| | | | | | | | | | | | | | | | | |
Db 1 tctccagcgtgcgccat 18

RESULT 9
AA278803 standard; DNA; 18 BP.
XX
XX AAX78803;
AC
XX 06-SEP-1999 (first entry)
DT
XX
XX HPV fusion protein Cpg oligonucleotide 2.
DE
XX
XX Fusion protein; E6 protein; E7 protein; immunomodulator; tumour;
KW immunological fusion partner; Cpg oligonucleotide; immune response;
KW HPV antigen; prevention; treatment; primer; ss.
XX
XX Synthetic.
OS Human papillomavirus.
XX
XX WO9933868-A2.
PN
XX
XX 08-JUL-1999.
PD
XX 18-DEC-1998; 98WO-EP08563.
PF
XX 24-DEC-1997; 97GB-0027262.
PR
XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
PI
XX
XX WPI: 1999-405485/34.
DR
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV
PT
XX
XX Claim 11; Page 37; 62pp; English.
PS
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used
CC for preventing or treating HPV induced tumours. This sequence represents
CC a Cpg oligonucleotide which is used in the method of the invention.
XX
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgccat 18
| | | | | | | | | | | | | | | | | |
Db 1 tctccagcgtgcgccat 18

RESULT 10
AAX88537 standard; DNA; 18 BP.
XX
XX AAX88537;
AC
XX
XX 10-SEP-1999 (first entry)
DT
XX
XX Cytosine-guanosine dinucleotide motif oligonucleotide #4.
DE
XX
XX Cytosine-guanosine dinucleotide motif; Cpg; immunomodulation;
KW unmethylated; vaccine; immunostimulation; immune response;
KW T-independent type 1 antigen; T-independent type 2 antigen;
KW polysaccharide conjugate antigen; ss.
XX
XX
XX Synthetic.
OS
XX
XX WO9933488-A2.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 18-DEC-1998; 98WO-EP08562.
PF
XX
XX 24-DEC-1997; 97GB-0027262.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Dalemans WLJ, Laferriere CAJ, Prieels J;
PI
XX
XX WPI: 1999-405369/34.
DR
XX
XX A vaccine composition for inducing an immune response to
PT T-independent type 1 or type 2 antigen or polysaccharide conjugate
PT antigen
PT
XX
XX Claim 6; Page 31; 35pp; English.
PS
XX
XX The present invention describes a formulation (A) comprising a
CC cytosine-guanosine dinucleotide motif (Cpg) oligonucleotide and
CC T-independent type 1 or type 2 antigens or polysaccharide conjugate
CC antigen. The present sequence represent a specifically claimed Cpg

CC oligonucleotide. A vaccine composition comprising the formulation is
CC used for inducing an immune response to T-independent type 1 or type 2
CC antigen or polysaccharide conjugate antigen. The use of
CC immunostimulatory CpG oligonucleotide acts as an adjuvant to
CC pneumococcal polysaccharides.
XX
SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. NO. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccagcgtgcgcacat 18
Db 1 tctccagcgtgcgcacat 18

RESULT 11

AA33514
ID AAX33514 standard; DNA; 18 BP.

XX AAX33514;

DT 07-JUL-1999 (first entry)

DE BCL2-targeted antisense oligonucleotide SEQ ID NO:45.

XX Combinatorial antisense library; oligonucleotide analogue; RNase;
XX ribozyme; cleavage; anchor; binding; target RNA; ss.

OS Synthetic.

PN WO9118238-A1.

PD 15-APR-1999.

PF 28-SEP-1998; 98WO-US20361.

PR 18-AUG-1998; 98US-0136080.

PR 02-OCT-1997; 97US-0060673.

PA (OASIS-) OASIS BIOSCIENCES INC.

PI Arnold LJ, Brown BD, Riley TA;

DR WPI; 1999-264039/22.

XX Oligonucleotide analog compositions capable of coupling to form
XX antisense molecules

PS Example 9; Page 45; 71pp; English.

CC The present invention describes a composition comprising two
CC oligonucleotide analogues, each having a binding domain and a coupling
CC moiety, where the binding domains are capable of hybridizing to a target
CC polynucleotide and the coupling moieties are capable of coupling to each
CC other in the absence of a target molecule. The composition/compound is
CC used to cleave an RNA target. The composition/compound is
CC an optimal antisense site for a given mRNA or an optimal ribozyme
CC cleavage site for a target RNA. By separating the antisense molecules
CC into two or more pieces, a comprehensive antisense library can be
CC prepared in advance, rather than synthesizing a plurality of candidate
CC antisense molecules as needed. A complete library of every possible
CC 17-mer oligonucleotide, using the four natural bases, would consist of
CC 417 (or about 1.7 x 10¹⁰) molecules. By providing the antisense molecules
CC in at least two components, e.g., a library of 8-mers and a library of
CC 9-mers, assembled quickly as needed, the library size is reduced to 48 +
CC 49, or 327 650 molecules. The complexity of the library can be further
CC reduced by substituting one or more universal or degenerate bases for
CC some of the natural bases. The present sequence represents an
XX oligonucleotide, which is used in an example from the present invention.

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. NO. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccagcgtgcgcacat 18
Db 1 tctccagcgtgcgcacat 18

RESULT 12

AA33693
ID AAX23693 standard; DNA; 18 BP.

XX AAX23693;

DT 18-JUN-1999 (first entry)

DE Deletion sequence oligonucleotide 146.

XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.

OS Synthetic.

PN WO911820-A1.

PD 11-MAR-1999.

PF 01-SEP-1998; 98WO-US18084.

PR 02-SEP-1997; 97US-0923771.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Srivatsa GS;

DR WPI; 1999-205198/17.

XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides

PS Example 9; Page 152; 163pp; English.

CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC compositions that are useful for modulating cellular pharmaceutical
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 13

AAK27536/c
 ID AAK27536 standard; RNA; 18 BP.

AC AAK27536;

DT 27-MAY-1999 (first entry)

DE Synthetic RNA sequence produced by the method of the invention.

KW Silyloxymethyl phosphonate; silyloxymethyl halide; diagnosis; ss;
 KM cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.

OS Synthetic.

PN WO9909044-A1.

PD 25-FEB-1999.

PF 17-AUG-1998; 98WO-EP05215.

PR 18-AUG-1997; 97CH-0001931.

XX (JENN/) JENNY L.

PA (PITS/) PITTSCH S.

PI (WEIS/) WEISS P A.

PI Jenny L, Pitsch S, Weiss PA;

DR WPI, 1999-180963/15.

2-silyloxymethyl ribonucleosides and their phosphonate derivatives

- have high purity, use in machine synthesis of ribonucleic acids,
 enable longer oligonucleotide chain construction, and larger amounts

Example 7: Page 26; 38pp; English.

The invention relates to silyloxymethyl protected D- or L-ribonucleosides and their phosphonates (I), and silyloxymethyl halides (II). (I) are intermediates for synthesis of RNA-oligonucleotides with predetermined nucleotide sequence, particularly by machine synthesis. The groups specified above, apart from those on silyl, are those particularly for the cyanoethyl phosphoramidate coupling. Uses of the oligonucleotide products in diagnosis, therapy, and as research tools, are well known, and are not dealt with in detail. (II) is an intermediate for (I). The silyloxymethyl halide reagent is easy to prepare, and yields are high. Introduction of the silyloxymethyl group into the ribonucleoside is simple and rapid, and the acetal bond formed does not migrate, eliminating particularly the prior art problem of 2' to 3' isomerisation. The methylenedioxy group spacer between the silyl group and nucleoside ring results in less steric hindrance than bulky direct silyloxy linkages, enabling firstly, a range of choices for the silyl substituents, to provide, e.g., acid or base stability; and second, higher yields in coupling. Purer products are therefore obtained than in prior art, enabling larger quantities and longer chains of oligoribonucleotides to be synthesised successfully, and in shorter times.

Sequence 18 BP; 4 A; 4 C; 8 G; 2 U; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 18 tctccagcgtgcgcacat 1

RESULT 14

AAK18702
 ID AAK18702 standard; DNA; 18 BP.

AC AAK18702;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide BCL-2.

KW Cellular adhesion protein; proliferation; antisense oligonucleotide;

KM alimentary canal; transport; gastrointestinal mucosa; cancer;

KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KW HIV; inflammation; ss.

OS Synthetic.

PN WO9901579-A1.

PD 14-JAN-1999.

PF 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

XX Hardee G, Teng C;

DR WPI, 1999-106077/09.

Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability

Example 2: Page 86; 115pp; English.
 A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAK1869 to AAK18793 and AAK18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 15
 AAV99434

Mon Jul 1 08:40:52 2002

us-09-709-170a-17.szm75.rng

1
2
3
4

5

6

7

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:53 ; Search time 334.55 Seconds
(without alignments)
13.216 Million cell updates/sec

Title: US-09-709-170A-17
Perfect score: 18
Sequence: 1 tctccagcgtcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_NA:*
2: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
3: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
5: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
6: /cgn2_6/prodata/1/lna/6C.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	1	US-08-217-082A-17
2	18	100.0	18	2	US-08-465-485A-17
3	18	100.0	18	2	US-08-465-485A-17
4	18	100.0	18	3	US-09-080-285-17
5	18	100.0	18	3	US-09-080-285-17
6	18	100.0	18	3	US-09-080-285-17
7	18	100.0	18	3	US-09-080-285-17
8	18	100.0	18	3	US-09-080-285-17
9	18	100.0	18	3	US-09-080-285-17
10	18	100.0	18	3	US-09-080-285-17
11	18	100.0	18	3	US-09-080-285-17
12	18	100.0	18	3	US-09-080-285-17
13	18	100.0	18	3	US-09-080-285-17
14	18	100.0	18	3	US-09-080-285-17
15	18	100.0	18	3	US-09-080-285-17
16	18	100.0	18	3	US-09-080-285-17
17	18	100.0	18	3	US-09-080-285-17
18	18	100.0	18	3	US-09-080-285-17
19	18	100.0	18	3	US-09-080-285-17
20	18	100.0	18	3	US-09-080-285-17
21	18	100.0	18	3	US-09-080-285-17
22	18	100.0	18	3	US-09-080-285-17
23	18	100.0	18	3	US-09-080-285-17
24	18	100.0	18	3	US-09-080-285-17
25	18	100.0	18	3	US-09-080-285-17
26	18	100.0	18	3	US-09-080-285-17
27	18	100.0	18	3	US-09-080-285-17

28	16.4	91.1	20	4	US-09-109-663-72	Sequence 72, Appl
29	15.4	85.6	33	3	US-08-650-726-1	Sequence 1, Appl
30	15	83.3	17	2	US-08-217-082A-8	Sequence 8, Appl
31	15	83.3	17	2	US-08-877-831-1	Sequence 1, Appl
32	14	77.8	17	1	US-08-217-082A-10	Sequence 10, Appl
33	13.8	76.7	31	1	US-08-726-136-19	Sequence 19, Appl
34	13.8	76.7	31	3	US-09-103-434-19	Sequence 19, Appl
35	13.8	76.7	31	3	US-09-687-594-19	Sequence 19, Appl
36	13.4	74.4	17	4	US-09-030-701-40	Sequence 40, Appl
37	13.4	74.4	17	4	US-09-286-098-71	Sequence 71, Appl
38	13.4	74.4	17	4	US-08-960-774-71	Sequence 71, Appl
39	13	72.2	20	1	US-08-217-082A-1	Sequence 1, Appl
40	13	72.2	20	1	US-08-217-082A-7	Sequence 7, Appl
41	13	72.2	20	2	US-08-465-485A-1	Sequence 1, Appl
42	13	72.2	20	3	US-08-465-485A-7	Sequence 7, Appl
43	13	72.2	20	3	US-09-080-285-1	Sequence 1, Appl
44	13	72.2	20	3	US-09-080-285-7	Sequence 7, Appl
45	13	72.2	20	4	US-09-379-718-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-217-082A-17
Sequence 17, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
US-08-217-082A-17

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 2
US-08-465-485A-17
Sequence 17, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Portney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-485A-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 3
US-08-465-485A-24
Sequence 24, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Portney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
phosphorothioates
US-08-465-485A-24

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 4
US-09-080-285-17
Sequence 17, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-080-285-17

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||

Db 1 TCTCCAGCGTGCGCACAT 18

RESULT 5
US-09-080-285-24
Sequence 24, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-09-080-285-24

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||

Db 1 TCTCCAGCGTGCGCACAT 18

RESULT 6
US-09-249-730-218
Sequence 218, Application US/09249730
Patent No. 6121000
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
FILE REFERENCE: 032396-040
CURRENT APPLICATION NUMBER: US/09/249,730
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 220
SOFTWARE: Patentln Ver. 2.0
SEQUENCE: Patentln Ver. 2.0
SEQ ID NO 218
LENGTH: 18
TYPE: DNA
ORGANISM: Human
US-09-249-730-218

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 7

US-09-118-220-1
; Sequence 1, Application US/09118220
; Patent No. 6140051
; GENERAL INFORMATION:
; APPLICANT: Brown, Lauren R.
; APPLICANT: Xu, Cheng
; TITLE OF INVENTION: FLUORESCENT DIBENZAZOLE DERIVATIVES
; TITLE OF INVENTION: AND METHODS RELATED THERETO
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/118,220
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfield, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/DOCKET NUMBER: GENTA.050A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-118-220-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 8

US-08-738-652-55
; Sequence 55, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15

; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-55

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 9

US-09-030-701-27
; Sequence 27, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 10

US-09-286-098-59
; Sequence 59, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-59

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 11
US-09-286-098-104
Sequence 104, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:
APPLICANT: Krieger, Arthur M.
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 104
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-104

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 12
US-08-960-774-45
Sequence 45, Application US/08960774
Patent No. 6239116
GENERAL INFORMATION:
APPLICANT: Krieger et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.,
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-960-774-45

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 13
US-09-078-954-14
Sequence 14, Application US/09078954
Patent No. 6287591
GENERAL INFORMATION:
APPLICANT: SEMPLER, Sean C.
APPLICANT: Klimuk, Sandra K.
APPLICANT: Harasym, Troy
APPLICANT: Hope, Michael J.
APPLICANT: Ansell, Steven M.
APPLICANT: Cullis, Pieter
APPLICANT: Scherrier, Peter
APPLICANT: Geisler, Timothy
APPLICANT: Zon, Gerald
APPLICANT: Debever, Dan
TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents
TITLE OF INVENTION: Lipid Vesicles
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,374
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: INEX.P-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2060
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHEICAL: no
ANTI-SENSE: yes
US-09-078-954-14

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 TCTCCAGCGTGCACCAT 18

RESULT 14
US-09-082-649B-60
Sequence 60, Application US/09082649B
Patent No. 633068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
APPLICANT: Krieger, Arthur M.
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
FILE REFERENCE: C1039/7008
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR FILING DATE: 1997-05-20
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-60

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 15
US-08-410-804-13/C
Sequence 13, Application US/08410804
Patent No. 5632994
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki

TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-410-804-13

Query Match 100.0%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 25 TCTCCAGCGTGCACCAT 8

Search completed: June 28, 2002, 22:16:53
Job time: 8279 sec

Mon Jul 1 08:40:52 2002

us-09-709-170a-17.szlm75.rni

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

Db 1 CGGAGCGCGCGCGCC 16

RESULT 2
AR032762/c
LOCUS AR032762
DEFINITION Sequence 374 from patent US 5869241.
ACCESSION AR032762
VERSION AR032762.1 GI:5948367
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 374 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..50
BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

Db 43 CGGAGCGCGCGCGCC 28

RESULT 3
LOCUS 129502/c
DEFINITION Sequence 374 from patent US 5578444.
ACCESSION 129502
VERSION 129502.1 GI:1820293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 374 26-NOV-1996;
FEATURES Location/Qualifiers
source 1..50
BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

Db 43 CGGAGCGCGCGCGCC 28

RESULT 4
LOCUS 191176/c
DEFINITION Sequence 374 from patent US 5726014.
ACCESSION 191176

50 bp DNA linear PAT 01-DEC-1998

VERSION 191176.1 GI:3935646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
TITLE Screening assay for the detection of DNA-binding molecules
JOURNAL Patent: US 5726014-A 374 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..50
BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

Db 43 CGGAGCGCGCGCGCC 28

RESULT 5
LOCUS AX008888
DEFINITION Sequence 3 from Patent WO964584.
ACCESSION AX008888
VERSION AX008888.1 GI:996309
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kramer,P. and Peter,M.
TITLE Protein for regulating apoptosis
JOURNAL Patent: WO 964584-A 3 16-DEC-1999;
FEATURES Location/Qualifiers
source 1..35
BASE COUNT 6 a 10 c 16 g 3 t
ORIGIN

Query Match 80.0%; Score 12.8; DB 6; Length 35;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

Db 9 CGGAGCATGGCGCGCC 24

RESULT 6
LOCUS S67824
DEFINITION envelope protein p43K [promoter] [Molluscum contagiosum virus subtype II MCV II, Genomic, 53 nt].
ACCESSION S67824
VERSION S67824.1 GI:544609
KEYWORDS
SOURCE Molluscum contagiosum virus subtype 2.
ORGANISM Molluscum contagiosum virus subtype 2.
REFERENCE 1 (bases 1 to 53)
AUTHORS Porter,C.D., Blake,N.W., Cream,J.J. and Archard,L.C.
TITLE Molluscum contagiosum virus

JOURNAL Mol Cell Biol. Hum. Dis. Ser. 1, 233-257 (1992)

MEDLINE 94084333
Genbank staff at the National Library of Medicine created this entry [NCBI g142099] from the original journal article.

REMARK This sequence comes from Fig. 8.5.

FEATURES Location/Qualifiers

source

1..53
/organism="Molluscum contagiosum virus subtype 2"

gene /db_xref="taxon:10281"

51..53
/partial
/gene="envelope protein p43k"

BASE COUNT 6 a 15 c 22 g 10 t

ORIGIN

Query Match 80.0%; Score 12.8; DB 14; Length 53;

Best Local Similarity 87.5%; Pred. No. 1.9e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggagcgcgcgcgcg 16

Db 1 CGGGCGCGCGCTGGC 16

RESULT 7

AX215485/c AX215485 17 bp mRNA linear PAT 07-SEP-2001

LOCUS Sequence 927 from Patent WO0159103.

ACCESSION AX215485

VERSION AX215485.1 GI:15525528

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 17)

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL nogo gene expression

PATENT: WO 0159103-A 927 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers

source 1..17

BASE COUNT 0 a 12 c 4 g 1 t

ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 17;

Best Local Similarity 92.9%; Pred. No. 3.7e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gggagcgcgcgcg 15

Db 17 GGGGCGCGCGCGG 4

RESULT 8

AX216149/c AX216149 17 bp mRNA linear PAT 07-SEP-2001

LOCUS Sequence 1591 from Patent WO0159103.

ACCESSION AX216149

VERSION AX216149.1 GI:15526192

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 17)

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL nogo gene expression

PATENT: WO 0159103-A 1591 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers

source 1..17

BASE COUNT 0 a 13 c 3 g 1 t

ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 17;

Best Local Similarity 92.9%; Pred. No. 3.7e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gggagcgcgcgcg 15

Db 16 GGGGCGCGCGCGG 3

RESULT 9

AX216150/c AX216150 17 bp mRNA linear PAT 07-SEP-2001

LOCUS Sequence 1592 from Patent WO0159103.

ACCESSION AX216150

VERSION AX216150.1 GI:15526193

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 17)

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL nogo gene expression

PATENT: WO 0159103-A 1592 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers

source 1..17

BASE COUNT 0 a 13 c 3 g 1 t

ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 17;

Best Local Similarity 92.9%; Pred. No. 3.7e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gggagcgcgcgcg 15

Db 14 GGGGCGCGCGCGG 1

RESULT 10

ARI39322/c ARI39322 20 bp DNA linear PAT 16-JUN-2001

LOCUS Sequence 30 from patent US 6207372.

ACCESSION ARI39322

VERSION ARI39322.1 GI:14481818

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Shuber, A.P.

TITLE Universal primer sequence for multiplex DNA amplification

JOURNAL Patent: US 6207372-A 30 27-MAR-2001;

FEATURES Location/Qualifiers

source 1..20

BASE COUNT 0 a 14 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 99agcgcgcgcgcgc 16
15 GGGGGCGGGCGGGC 2

RESULT 11
LOCUS AR003393/c 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 28 from patent US 5744306.
ACCESSION AR003393
VERSION AR003393.1 GI:3964652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J., Jr. and Thunnissen,F.B.J.M.
TITLE Methods for nucleic acid detection, sequencing, and cloning using
exonuclease
JOURNAL Patent: US 5744306-A 28 28-APR-1998;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"

BASE COUNT 0 a 15 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 99agcgcgcgcgcgc 16
15 GGGGGCGGGCGGGC 2

RESULT 12
LOCUS I21182/c 21 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 28 from patent US 5518901.
ACCESSION I21182
VERSION I21182.1 GI:1601536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J.
TITLE Methods for adapting nucleic acid for detection, sequencing, and
cloning using exonuclease
JOURNAL Patent: US 5518901-A 28 21-MAY-1996;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"

Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 99agcgcgcgcgcgc 16
15 GGGGGCGGGCGGGC 2

Db 15 GGGGGCGGGCGGGC 2

RESULT 13
LOCUS I74449/c 21 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 28 from patent US 5688669.
ACCESSION I74449
VERSION I74449.1 GI:3010590
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J.
TITLE Methods for nucleic acid detection, sequencing, and cloning using
exonuclease
JOURNAL Patent: US 5688669-A 28 18-NOV-1997;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"

BASE COUNT 0 a 15 c 6 g 0 t
ORIGIN

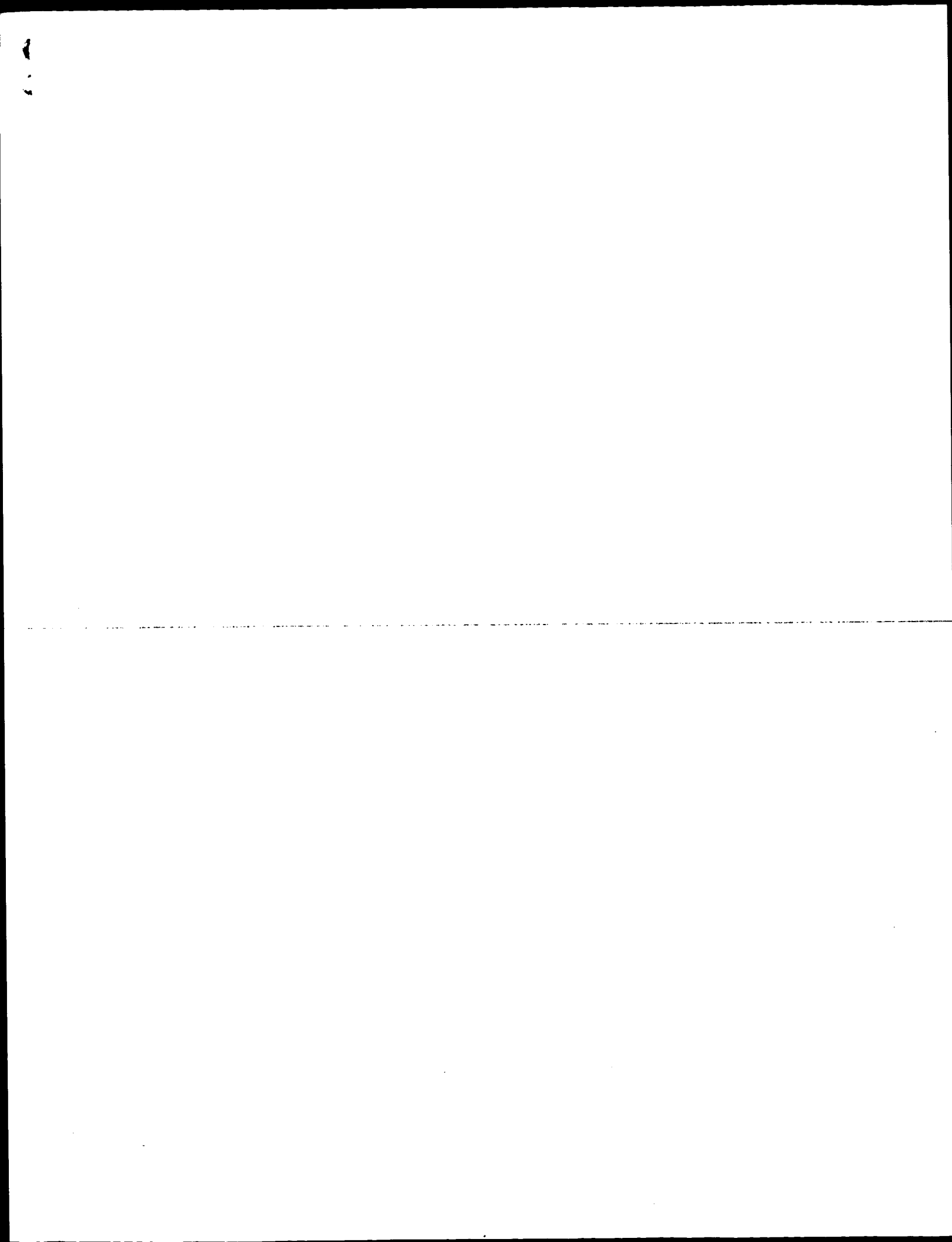
Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 99agcgcgcgcgcgc 16
15 GGGGGCGGGCGGGC 2

RESULT 14
LOCUS AX249410 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1489 from Patent WO0166800.
ACCESSION AX249410
VERSION AX249410.1 GI:15864033
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Gargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1489 13-SEP-2001;
FEATURES
source Location/Qualifiers
1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2 a 9 c 16 g 3 t 1 others
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 31;
Best Local Similarity 81.2%; Pred. No. 3.2e+05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 1 99agcgcgcgcgcgc 16
2 CCGGAGCGGGGTGKC 17

RESULT 15
LOCUS A51123/c 50 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 1 from Patent WO9617081.
ACCESSION A51123
VERSION A51123.1 GI:2303898



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OM nucleic - nucleic search, using sw model

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Run on:      June 28, 2002, 22:40:19 ; Search time 1381.16 Seconds
              (Without alignments)
              19.890 Million cell updates/sec
```

Title:	US-09-709-170A-16
Perfect score:	16
Sequence:	1 cgggagcgcgcgcggc 16

Scoring table:	IDENTITY_NUC	Gapext 1.0
Gapop 10.0		

```
Searched:      1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters: 1996432
```

```
Minimum DB seq length: 0
Maximum DB seq length: 75
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
N_Genseq_032802.*
1:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
13:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
14:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
15:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
16:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
17:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
18:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
19:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
20:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
21:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
22:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
23:/SDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	100.0	15	16	AA086658	Bcl-2 antisense 01
2	16	100.0	16	19	AAV28180	Antisense oligonucleotide
3	16	100.0	16	20	AAK23692	Deletion sequence
4	16	100.0	16	20	AAK18701	Target bcl-2 antisense
5	16	100.0	50	15	AA069624	Human bcl-2 proto-oncogene
c	16	100.0	50	18	AAAT64086	Human B-cell leukemia
c	16	100.0	50	20	AAK17374	Test sequence from human
8	13.6	85.0	65	21	AAK1547	Human secreted protein
9	13.4	83.8	67	21	AAK11202	Human secreted protein

10	12.6	80.0	25	17	AA742053	Exotoxin A gene PC
11	12.8	80.0	31	22	AA131001	Human single nucle
12	12.8	80.0	35	21	AA439325	Murine DEBD PCR pr
13	12.8	80.0	38	12	AAQ14201	Probe p1672 for GI
14	12.8	80.0	47	20	AA552519	PCR primer for In
15	12.8	80.0	47	22	AAE72719	Human PRO polypept
16	12.8	80.0	47	22	AA597550	Human PRO258 In si
17	12.8	80.0	47	22	AA561402	Mouse Clock gene e
18	12.8	80.0	71	19	AA739143	IGF-I oligonucleot
19	12.4	77.5	15	22	AAE49144	IGF-I oligonucleot
20	12.4	77.5	17	23	ABK00927	Human NOGO Inozyme
21	12.4	77.5	17	23	ABK01591	Human NOGO G-Cleav
22	12.4	77.5	17	23	ABK01592	Human NOGO G-Cleav
23	12.4	77.5	20	18	AA747373	Human NOGO 49 of uni
24	12.4	77.5	21	16	AAO78952	Gene-specific prim
25	12.4	77.5	21	18	AA780851	Gene-specific prim
26	12.4	77.5	24	21	AAZ29432	Gene specific prim
27	12.4	77.5	33	21	AAA60889	PCR primer JCI17 f
28	12.4	77.5	33	17	AA103676	Mouse cystatin C p
29	12.4	77.5	47	18	AA733790	Hepatitis C diagno
30	12.4	77.5	49	18	AA733806	Multiplex short-PC
31	12.4	77.5	49	18	AA733766	Multiplex short-PC
32	12.4	77.5	50	17	AA728823	Multiplex short-PC
33	12.4	77.5	50	18	AA73736	PCR primer for HTR
34	12.4	77.5	50	18	AA73801	Multiplex short-PC
35	12.4	77.5	50	18	AA73804	Multiplex short-PC
36	12.4	77.5	50	18	AA737681	Multiplex short-PC
37	12.4	77.5	50	18	AA73782	Multiplex short-PC
38	12.4	77.5	50	18	AA73788	Multiplex short-PC
39	12.4	77.5	50	18	AA73770	Multiplex short-PC
40	12.4	77.5	50	18	AA73774	Multiplex short-PC
41	12.4	77.5	50	18	AA73762	Multiplex short-PC
42	12.4	77.5	50	18	AA73764	Multiplex short-PC
43	12.4	77.5	50	18	AA73764	Human SNP oligonuc
44	12.4	77.5	50	22	AA130181	Human SNP oligonuc
45	12.4	77.5	50	22	AA134074	Human SNP oligonuc

ALIGNMENTS

RESULT	1
AAQ86658	
ID	AAQ86658 standard; DNA; 16 BP.

AC	AAQ86658;
XX	
DT	27-SEP-1995 (first entry)

Bcl-2 antisense oligonucleotide.

AA Anticodone oligomer; antisense oligonucleotide; bcl-2; cancer; therapy
 KW lymphoma; programmed cell death; ss.
 KW lymphoma; programmed cell death; ss.

OS Synthetic.

Key	Location/Qualifiers
FH	1..16
FT	/*tag= a
FT	/note= "3'-5' (antisense) sequence"
FT	

PN	W09508350 -A.	
XX		
PD	30-MAR-1995.	
XX		
PF	20-SEP-1994;	94MO-US10725
XX		
PR	20-SEP-1993;	93US-0124256
XX		
PA	(REED/) REED J C.	
XX		
PI	Reed JC;	
XX		

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086550-55) or the 5'-cap
CC region (AA086556-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 16 BP; 1 A; 5 C; 10 G; 0 T; 0 other;

Query Match 100.0%; Score 16; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgggagcgcgcgcgcg 16
|||||
Db 1 cgggagcgcgcgcgcgcg 16

RESULT 2

AAV28180
ID AAV28180 standard; DNA; 16 BP.

AC AAV28180;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

XX WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97WO-US3284.

PR 19-DEC-1996; 96US-0769951.

XX (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 85; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides. Specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match 100.0%; Score 16; DB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgggagcgcgcgcgcg 16
|||||
Db 1 cgggagcgcgcgcgcgcg 16

RESULT 3

AAV23692
ID AAV23692 standard; DNA; 16 BP.

AC AAV23692;

DT 18-JUN-1999 (first entry)

DE Deletion sequence oligonucleotide 145.

KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.

OS Synthetic.

XX WO9911820-A1.

PD 11-MAR-1999.

PF 01-SEP-1998; 98WO-US18084.

PR 02-SEP-1997; 97US-0923771.

XX (ISIS-) ISIS PHARM INC.

PI Chen D, Srivatsa GS;

DR WPI; 1999-205198/17.

PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides

PS Example 9; Page 152; 163pp; English.

CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match 100.0%; Score 16; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||
DB 1 cggagagcgcgcgcgcc 16

RESULT 4

AA18701
ID AAX18701 standard; DNA; 16 BP.

AC AAX18701;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #33.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KW HIV; inflammation; ss.

OS Synthetic.

PN MO9901579-A1.

PD 14-JUN-1999.

PF 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

PS (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

PT WPI; 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability

PS Example 2; Page 86; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases the stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAX18669 to AAX18799 and AAX18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

CC Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 16; DB 20; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||
DB 1 cggagagcgcgcgcgcc 16

RESULT 5

AA069624/C
ID AA069624 standard; DNA; 50 BP.

AC AA069624;

DT 01-MAR-1995 (first entry)

DE Human bcl-2 proto-oncogene, target region.

XX DNA protein-binding assay; test sequence; screening sequence;

KW promoter; target; TATA box; Herpes Simplex Virus; HSV;

KW origin of replication; UL9; transcription factor; TRITD: ds.

OS Synthetic.

PN WO9414980-A.

PD 07-JUL-1994.

PF 20-DEC-1993; 93WO-US12388.

PR 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

PS (GENE-) GENELABS TECHNOLOGIES INC.

PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

PT WPI; 1994-234711/28.

PS Sequence-directed DNA-binding molecules - useful in pharmaceuticals and as molecular reagents

PS Claim 28; Page 399; 587pp; English.

CC A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpos. For their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein-binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a mol. binds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is to eucaryotic general transcription factors (e.g. TFIID), where the target region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary test sequences are given: the sequences in AA069251-731 and AA069850 correspond to promoter targets (typically, TATA box-contg. sites) for human genes and the sequences in AA069732-849 correspond to promoter targets for viral genes. The test sequences may also be randomly generated. DNA:protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AA069851-52, AA069865 and AA069891).

CC Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 16; DB 15; Length 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||
DB 43 CGGAGAGCGCGCGCGCC 28

RESULT 6

AA064086/C
ID AA064086 standard; DNA; 50 BP.

XX AAT64086;
AC
XX 14-MAR-1997 (first entry)
DT
XX Human B-cell leukemia/lymphoma 2 protooncogene TFIID binding site.
DE
XX Duplex DNA; target region; binding characteristic; DNA binding protein;
KM TFIID; transcription factor; binding site; inhibition; enhance;
KM cancer; inherited genetic disorder; ds.
XX
XX Homo sapiens.
OS
XX US5578444-A.
PN
XX 26-NOV-1996.
PD
XX 27-JUN-1991; 91US-0723618.
PF
XX 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
PI
XX WPI; 1997-020402/02.
DR
XX
XX Altering binding characteristics of DNA binding proteins to duplex
PT DNA - by attaching specific small cpd. to target region close to the
PT protein's binding site, useful in treatment of viral disease, cancer
PT etc
XX
XX Claim 6; Column 289; 264pp; English.
PS
XX The sequences given in AAT63713-4312 represent duplex DNA's which act
XX as target regions in the method of the invention. The method for
CC altering the binding characteristics of a DNA-binding protein to duplex
CC DNA comprises contacting the duplex DNA with a small molecule which
CC binds sequence-specifically to a target region, where, when the small
CC molecule is bound to the target region, it is adjacent to, but not
CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
CC The small molecule is added at a concentration effective to alter the
CC binding of the DNA binding protein, pref. TFIID, to its binding site on
CC the duplex DNA. The binding of the small molecule may inhibit or
CC enhance the binding of the DNA-binding protein to its binding site. The
CC compounds isolated using this method are potentially useful as
CC therapeutic agents for treatment of any disease which involves a
CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
CC The method is suitable for screening large biological or chemical
CC libraries and allows determination of sequence-specific and relative
CC affinities of known DNA-binding agents for different DNA sequences.
CC The design of these duplex DNA's allows a single DNA-protein interaction
CC to be used for screening sequence-specific, or preferential, DNA binding
CC proteins that recognise almost any possible sequence (see also AAT9539-
CC 74).
XX
XX Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 16; DB 18; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
|||||
Db 43 CGGAGAGCGCGCGGCGC 28

RESULT 7
AAx17374/c

ID AAX17374 standard; DNA; 50 BP.
XX
XX AAX17374;
AC
XX 06-MAY-1999 (first entry)
DT
XX Test sequence from B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene.
DE
XX Test sequence; DNA-binding molecule; screening sequence; human;
KM nucleic acid amplification; target; viral; ds.
KM
XX
XX Homo sapiens.
OS
XX US5869241-A.
PN
XX 09-FEB-1999.
PD
XX 07-JUN-1995; 95US-0475228.
PF
XX 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
PR 07-JUN-1995; 95US-0475228.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
PI
XX WPI; 1999-152755/13.
DR
XX
XX Determination of DNA sequence preference of a DNA-binding molecule -
PT based on inhibition of binding of protein to oligonucleotide
PT sequence attached to test sequence
PT
XX
XX Claim 3; Columns 291-292; 270pp; English.
PS
XX Sequences AAX17001 to AAX17600 represent specifically claimed target
XX test sequences that are used in the method of the invention of
CC determining the DNA sequence preference of a DNA-binding molecule. The
CC method comprises: (i) adding a test molecule and a DNA-binding protein to
CC a mixture of duplex DNA test oligonucleotides, each of the test
CC oligonucleotides having a test sequence adjacent to a screening sequence,
CC where the screening sequence binds to the DNA-binding protein with a
CC binding affinity that is independent of the DNA sequence of the test
CC sequence, and where the mixture of duplex DNA test oligonucleotides
CC includes several test sequences; (ii) incubating the test molecule, the
CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
CC for a time sufficient to permit binding of the test molecule to test
CC sequences in the duplex DNA; (iii) separating unbound test
CC oligonucleotides from test oligonucleotides bound to binding protein;
CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
CC (vii) sequencing the isolated test oligonucleotides. Test sequences
CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
CC genes and test sequences AAX17482-X17599 correspond to promoter targets
CC for viral genes.
XX
XX Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 16; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
|||||
Db 43 CGGAGAGCGCGCGGCGC 28

RESULT 8
AAC31547
ID AAC31547 standard; cDNA; 66 BP.


```

XX AC AAC31547;
XX 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 35622.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KM gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PI EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PS (GEST ) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI: 2000-500381/45.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 1; SEQ ID 35622; 71pp + CD-ROM; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.
XX SQ Sequence 66 BP; 9 A; 27 C; 20 G; 8 T; 2 other;

Query Match 85.0%; Score 13.6; DB 21; Length 66;
Best Local Similarity 81.2%; Pred. No. 3.2e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgggagcgcgcggc 16
   ||||| |||||
DB 5 cgggagcgcgcggc 20

RESULT 9
AAC11202
ID AAC11202 standard; cDNA; 67 BP.
AC AAC11202;
XX 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 15277.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KM gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.

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XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PS (GEST ) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI: 2000-500381/45.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 1; SEQ ID 15277; 71pp + CD-ROM; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.
XX SQ Sequence 67 BP; 11 A; 21 C; 29 G; 6 T; 0 other;

Query Match 83.8%; Score 13.4; DB 21; Length 67;
Best Local Similarity 93.3%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgggagcgcgcggc 15
   ||||| |||||
DB 29 cgggagcgcgcggc 43

RESULT 10
AAT42053
ID AAT42053 standard; DNA; 25 BP.
AC AAT42053;
XX 29-JAN-1997 (first entry)
XX DE Exotoxin A gene PCR primer.
XX KW Exotoxin A; ETA; cytotoxin; Pseudomonas aeruginosa;
XX KM single chain antibody; scFv; monoclonal antibody; MA; EGF;
XX KM epidermal growth factor; receptor; cancer; therapy; antitumour;
XX KM polymerase chain reaction; PCR; primer; ss.
XX OS Synthetic.
XX PI EP739984-A1.
XX PD 30-OCT-1996.
XX PF 26-APR-1995; 95EP-0106275.
XX PR 26-APR-1995; 95EP-0106275.
XX PS

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PA (SANT-) SAN TUMORFORSCHUNGS GMBH.
 XX
 PI Groner B, Schmidt M, Wels W;
 XX
 DR WPI; 1996-478748/48.
 XX
 PT Bivalent fusion proteins that bind epidermal growth factor receptor
 PT or analogues - and comprise at least two different cell surface
 PT binding domain(s), useful for tumour therapy
 XX
 XX Example 9.4; Page 10; 52pp; English.
 XX
 CC PCR primers (AA131001 and AA131002) were designed to amplify a
 CC portion of the exotoxin A (ETA) gene of Pseudomonas aeruginosa
 CC coding for amino acids 380-613 of the ETA protein. Plasmid pMW20
 CC was used as template. Another primer pair (AA131001-52) was
 CC used to amplify DNA coding for ETA amino acids 252-366. The
 CC amplified fragments can be adapted for insertion into novel
 CC bacterial expression vectors (see also AA131001-44) coding
 CC for bivalent proteins (AA131001-44) that include the cytotoxin ETA.
 CC These fusion proteins are useful as antitumour agents.
 XX
 CC Sequence 25 BP; 1 A; 9 C; 13 G; 2 T; 0 other;
 XX
 S0
 Query Match 80.0%; Score 12.8; DB 17; Length 25;
 Best Local Similarity 87.5%; Pred. No. 8e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cggagagcgcgcgagc 16
 ||||||| |||||
 Db 3 cggagagcgcgcgagc 18
 RESULT 11
 AA131001
 ID AA131001 standard; DNA; 31 BP.
 XX
 AC AA131001;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human single nucleotide polymorphism (SNP) 218.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,T)
 FT /tag=a
 FT /standard_name="single nucleotide polymorphism"
 XX
 PN WO200166800-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US07268.
 XX
 PR 07-MAR-2000; 2000US-0187510.
 PR 22-MAY-2000; 2000US-0206129.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or
 PT severity of a particular phenotype or disorder (e.g. diabetes)
 PT associated with a particular genotype -

XX
 PS Claim 1; Page 122; 145pp; English.
 XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AA131001-AA131002) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.
 XX
 S0
 Sequence 31 BP; 2 A; 9 C; 17 G; 3 T; 0 other;
 XX
 S0
 Query Match 80.0%; Score 12.8; DB 22; Length 31;
 Best Local Similarity 87.5%; Pred. No. 7.8e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cggagagcgcgcgagc 16
 ||||||| |||||
 Db 2 cggagagcgcgcgagc 17
 RESULT 12
 AA243925
 ID AA243925 standard; DNA; 35 BP.
 XX
 AC AA243925;
 XX
 DT 17-MAR-2000 (first entry)
 XX
 DE Murine DEDD PCR primer 1.
 XX
 KW DEDD; murine; apoptosis; protein biosynthesis inhibitor; CD95;
 KW PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN DE19825621-A1.
 XX
 PD 09-DEC-1999.
 XX
 PF 08-JUN-1998; 98DE-1025621.
 XX
 PR 08-JUN-1998; 98DE-1025621.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Peter M, Krammer P;
 XX
 DR WPI; 2000-063547/06.
 XX
 PF New protein for regulating apoptosis, particularly for diagnosis or
 PF treatment of e.g. tumors and acquired immune deficiency syndrome -
 XX
 PS Example 1; Column 4; 12pp; German.
 XX
 CC This invention describes a novel DEDD protein (I) for regulating
 CC apoptosis which has antitumor and antiviral activity. (I) is expressed
 CC ubiquitously and after induction of the CD95 apoptotic signaling pathway
 CC migrates to the nucleus/nucleolus where it inhibits transcription of
 CC ribosomal DNA, and thus biosynthesis of proteins, including those with
 CC anti-apoptotic activity. (I) or the DNA (II), encoding it, is used for
 CC regulation and diagnostic detection of apoptosis, particularly in cases
 CC of disease, e.g. of the immune system (e.g. acquired immune deficiency
 CC syndrome) and tumors, also for studying apoptosis or its regulation.
 CC Antibodies (Ab) specific for (I) are used to detect/quantify (I).
 CC particularly as a function of time, also for inhibition of (I). (I) is
 CC used to raise Ab and for detection of specific autoantibodies. (II), or
 CC derived primers, can be used to detect expression and organization of
 CC the corresponding gene, also for inducing expression of (I) in vivo or

CC in selected tissues. This sequence represents a PCR primer used in
CC the amplification of the murine DEDD protein described in the method of
CC the invention.

XX Sequence 35 BP; 6 A; 10 C; 16 G; 3 T; 0 other;

Query Match 80.0%; Score 12.8; DB 21; Length 35;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cggagagcgagcgagc 16
||||| |||||
Db 9 cggagagcgagcgagc 24

RESULT 13
AAQ14201/c
ID AAQ14201 standard; DNA; 38 BP.

XX AAQ14201;

DT 10-JAN-1992 (first entry)

XX Probe P1672 for Giardia lamblia 18S rRNA.

XX Ribosomal RNA; diarrhoea; ss.

XX Synthetic.

OS EPA53290-A.

PN 23-OCT-1991.

PD 18-APR-1991; 91EP-0303479.

XX 18-APR-1990; 90US-0510476.

XX (GENE-) GENE-TRAK SYSTEM CORPORATION.

XX Shah JS, Buharin A, Lane DJ;

DR WPI, 1991-312505/43.

PT 18S ribosomal DNA or RNA nucleic acid probes - for the specific and
PT accurate detection of Giardia lamblia.

XX Claim 1; Fig 1; 32pp; English.

CC The probe hybridises to a region of the G. lamblia 18S rRNA which
CC starts at position corresponding to the region between bases
CC 500-409 of the E. coli sequence. It can be used for the detection
CC of this parasite which is a common cause of diarrhoea.
CC See also AAQ14197-Q14203.

XX Sequence 38 BP; 0 A; 16 C; 17 G; 5 T; 0 other;

Query Match 80.0%; Score 12.8; DB 12; Length 38;
Best Local Similarity 87.5%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cggagagcgagcgagc 16
||||| |||||
Db 36 CGCAGCGAGCGCGGC 21

RESULT 14
AAK52519/c
ID AAK52519 standard; DNA; 47 BP.

XX AAK52519;

DT 25-JUN-1999 (first entry)

XX PCR primer for in situ analysis of DNA35918-1174.

XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
XX fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
XX anti-thrombotic; wound healing; tissue repair; PCR primer; ss.

XX Synthetic.

PN WO914328-A2.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WO-US19330.

XX 25-NOV-1997; 97US-0066840.

XX 17-SEP-1997; 97US-0059113.

XX 17-SEP-1997; 97US-0059115.

XX 17-SEP-1997; 97US-0059117.

XX 17-SEP-1997; 97US-0059119.

XX 17-SEP-1997; 97US-0059121.

XX 17-SEP-1997; 97US-0059184.

XX 18-SEP-1997; 97US-0059263.

XX 18-SEP-1997; 97US-0059266.

XX 15-OCT-1997; 97US-0062125.

XX 17-OCT-1997; 97US-0062285.

XX 21-OCT-1997; 97US-0063886.

XX 24-OCT-1997; 97US-0062814.

XX 24-OCT-1997; 97US-0062816.

XX 24-OCT-1997; 97US-0063045.

XX 24-OCT-1997; 97US-0063120.

XX 24-OCT-1997; 97US-0063121.

XX 24-OCT-1997; 97US-0063127.

XX 24-OCT-1997; 97US-0063128.

XX 27-OCT-1997; 97US-0063329.

XX 28-OCT-1997; 97US-0063327.

XX 28-OCT-1997; 97US-0063541.

XX 28-OCT-1997; 97US-0063542.

XX 28-OCT-1997; 97US-0063544.

XX 28-OCT-1997; 97US-0063549.

XX 28-OCT-1997; 97US-0063550.

XX 29-OCT-1997; 97US-0063435.

XX 29-OCT-1997; 97US-0063704.

XX 29-OCT-1997; 97US-0063732.

XX 29-OCT-1997; 97US-0063738.

XX 29-OCT-1997; 97US-0063734.

XX 29-OCT-1997; 97US-0064215.

XX 29-OCT-1997; 97US-0063735.

XX 31-OCT-1997; 97US-0063870.

XX 31-OCT-1997; 97US-0064103.

XX 03-NOV-1997; 97US-0064248.

XX 07-NOV-1997; 97US-0064809.

XX 12-NOV-1997; 97US-0065186.

XX 17-NOV-1997; 97US-0065846.

XX 18-NOV-1997; 97US-0065693.

XX 21-NOV-1997; 97US-0066120.

XX 21-NOV-1997; 97US-0066364.

XX 24-NOV-1997; 97US-0066772.

XX 24-NOV-1997; 97US-0066466.

XX 24-NOV-1997; 97US-0066770.

XX 24-NOV-1997; 97US-0066511.

XX 24-NOV-1997; 97US-0066453.

(GENE) GENENTECH INC.

PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 XX WPI; 1999-229533/19.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration
 PS
 XX Example 74; Page 179; 320pp; English.
 CC Oligonucleotides AAX52276-532 represent PCR primers and probes used
 CC to isolate and amplify cDNA encoding secreted and transmembrane human
 CC proteins (see AAX52213-74 and AAX1344-403). The cDNA sequences are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
 CC have specific uses based on their homology to known polypeptides,
 CC e.g. PRO211 and PRO217 can be used for disorders associated with the
 CC preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal
 CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
 CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
 CC cell growth and development, diseases related to growth or survival of
 CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS, for
 CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
 CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
 CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
 CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
 CC polypeptides and portions may have therapeutic applications in wound
 CC healing and tissue repair; PRO317 can be used for treating problems of
 CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
 CC in the heart of genital tract.
 XX
 SQ Sequence 47 BP; 8 A; 17 C; 10 G; 12 T; 0 other;

Query Match 80.0%; Score 12.8; DB 20; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagagcgagcgagc 16
 I | | | | | | | | | |
 Db 41 CAGGAGCGAGCGCGGC 26

RESULT 15
 AAF72719/c
 ID AAF72719 standard; DNA; 47 BP.
 XX
 AC AAF72719;
 XX
 XX 24-APR-2001 (first entry)
 XX
 DE Human PRO polypeptide gene oligonucleotide SEQ ID NO: 362.
 XX
 KW Human; PRO; dermatological; antiproliferic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerrary; cardianc;
 KW antiangiogenic; vasotropic; antiasthmatic; antineumatic; cancer;
 KW antialtritic; antiliferility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischemia; inflammation; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US04414.
 XX
 XX 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.

PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US23214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 99WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gimaldi CJ, Gurney AL, Hillan KJ, Kljavn II;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-081051/09.
 XX
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 PS
 XX Example 102; Page 247; 393pp; English.

The present sequence is a probe which was used in the isolation of one
 CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful for treating skin diseases
 CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. lung squamous cell carcinoma),
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischemias such as coronary ischemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping.

SQ Sequence 47 BP; 8 A; 17 C; 10 G; 12 T; 0 other;

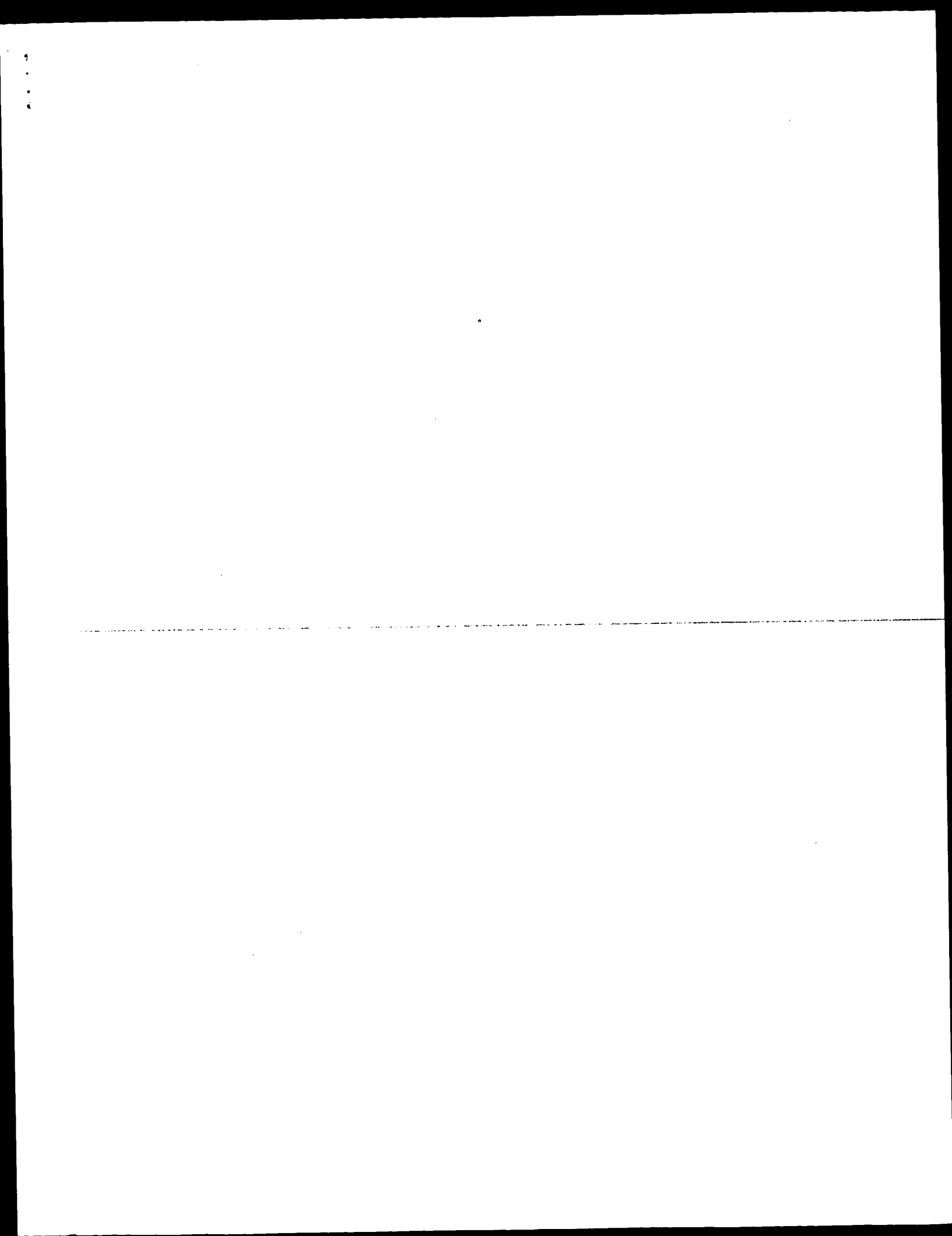
Query Match 80.0%; Score 12.8; DB 22; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagagcgagcgagc 16
 I | | | | | | | | | |
 Db 41 CAGGAGCGAGCGCGGC 26

Search completed: June 28, 2002, 22:40:21
 Job time: 8097 sec

Mon Jul 1 08:40:51 2002

us-09-709-170a-16.sz1m75.rng



Query Match 100.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cggagagcgagcgagc 16
|||||
Db 1 CGGAGAGCGGCGGCGC 16

RESULT 2
US-09-080-285-16
Sequence 16, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-16

Query Match 100.0%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cggagagcgagcgagc 16
|||||
Db 1 CGGAGAGCGGCGGCGC 16

RESULT 3
US-08-171-389-374/c
Sequence 374, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Tulin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/Lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
US-08-171-389-374

Query Match 100.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cggagagcgagcgagc 16
|||||
Db 43 CGGAGAGCGGCGGCGC 28

RESULT 4
US-08-123-936-374/C
Sequence 374, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
NUMBER OF SEQUENCES: 640
TITLE OF INVENTION: DNA-Binding Molecules
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
US-08-123-936-374
Query Match 100.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cggagagcgagcgagc 16
|||||
DB 43 CGGAGCGCGCGCGGC 28
RESULT 5
US-08-475-228A-374/C
Sequence 374, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.

APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
US-08-475-228A-374
Query Match 100.0%; Score 16; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cggagagcgagcgagc 16
|||||
DB 43 CGGAGCGCGCGCGGC 28
RESULT 6
US-08-482-080A-374/C
Sequence 374, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
US-08-482-080A-374

Query Match 100.0%; Score 16; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cggagcgcgcgcgcg 16
|||||
Db 43 CGGAGCGCGCGCGGC 28

RESULT 7
PCT-US93-12388-374/c
Sequence 374, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City

STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
PCT-US93-12388-374

Query Match 100.0%; Score 16; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cggagcgcgcgcgcg 16
|||||
Db 43 CGGAGCGCGCGCGGC 28

RESULT 8
US-08-983-466-30/c
Sequence 30, Application US/08983466
Patent No. 6207372
GENERAL INFORMATION:
APPLICANT: SHUBER, ANTHONY P.
TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,466
FILING DATE: 10-FEB-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,450
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W096/41012
FILING DATE: 06-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GECO.001.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
US-08-983-466-30

Query Match 77.5%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgagc 16
|||
Db 15 GGGCGCGCGCGGC 2

RESULT 9
US-08-049-264C-28/C
Sequence 28, Application US/0804264C
Patent No. 5518901
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
TITLE OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,264C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-049-264C-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgagc 16
|||
Db 15 GGGCGCGCGCGGC 2

RESULT 10
US-08-476-562-28/C
Sequence 28, Application US/08476562
Patent No. 5688669
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
TITLE OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,264
FILING DATE: April 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-562-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgagc 16
|||
Db 15 GGGCGCGCGCGGC 2

RESULT 11
US-08-479-723A-28/C
Sequence 28, Application US/08479723A
Patent No. 5744306
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.

TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
STREET: Peachtree Street N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,723A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 05010.0061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-479-723A-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 12
PCT-US94-04310-28/C
Sequence 28, Application PC/TUS9404310
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 74
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04310
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,264
FILING DATE: 19-APR-1993
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-04310-28

Query Match 77.5%; Score 12.4; DB 5; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 13
US-09-677-045-10/C
Sequence 10, Application US/09677045
Patent No. 6346386
GENERAL INFORMATION:
APPLICANT: Elenitoba-Johnson, Koji
TITLE OF INVENTION: Method of Solution-based Scanning for Alterations in a
TITLE OF INVENTION: DNA Segment Using a Double-stranded DNA Binding Dye and
TITLE OF INVENTION: Fluorescence Melting Profiles
FILE REFERENCE: 2379.2.5
CURRENT APPLICATION NUMBER: US/09/677,045
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO: 10
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-677-045-10

Query Match 77.5%; Score 12.4; DB 4; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.6e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 14
US-08-049-264C-7/C
Sequence 7, Application US/08049264C
Patent No. 5518901
GENERAL INFORMATION:
APPLICANT: Murrigh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
STREET: Peachtree Street N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,264C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.001
TELECOMMUNICATION INFORMATION:

Mon Jul 1 08:40:51 2002

us-09-709-170a-16.szlm75.rml

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:51 ; Search time 334.55 Seconds
(without alignments)
11.013 Million cell updates/sec

Title: US-09-709-170A-15
Perfect score: 15
Sequence: 1 cgcgcggcgacgca 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_NA:*
1: /cgn2_6/pdata/1/ina/5A.COMB.seq:*
2: /cgn2_6/pdata/1/ina/5B.COMB.seq:*
3: /cgn2_6/pdata/1/ina/6A.COMB.seq:*
4: /cgn2_6/pdata/1/ina/6B.COMB.seq:*
5: /cgn2_6/pdata/1/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/pdata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	2	US-08-465-485A-15
2	15	100.0	15	3	US-09-080-285-15
3	13.4	89.3	69	2	US-08-343-443B-46
4	12.4	82.7	17	6	5262866-3
5	11.8	78.7	18	2	US-08-519-300-2
6	11.8	78.7	24	1	US-08-002-024B-11
7	11.8	78.7	52	4	US-09-450-656-14
8	11.4	76.0	30	4	US-09-150-900-32
9	11.4	76.0	38	4	US-09-499-884-12
10	11.4	76.0	41	5	PCT-US95-10973A-55
11	11.4	76.0	45	1	US-08-171-389-300
12	11.4	76.0	45	1	US-08-133-936-300
13	11.4	76.0	45	2	US-08-475-228A-300
14	11.4	76.0	45	3	US-08-482-080A-300
15	11.4	76.0	45	5	PCT-US93-12388-300
16	11.4	76.0	56	5	PCT-US95-10973A-56
17	11.4	73.3	18	3	US-09-487-444-15
18	10.8	72.0	18	2	US-08-739-401A-1
19	10.8	72.0	18	2	US-08-602-264A-4
20	10.8	72.0	18	2	US-08-602-264A-5
21	10.8	72.0	18	2	US-09-205-860-9
22	10.8	72.0	18	3	US-08-461-018A-4
23	10.8	72.0	18	3	US-08-461-018A-5
24	10.8	72.0	18	4	US-09-216-958-4
25	10.8	72.0	18	4	US-09-216-958-5
26	10.8	72.0	22	4	US-09-398-217-1
27	10.8	72.0	22	4	US-09-562-331-1

28	10.8	72.0	25	1	US-08-510-032A-5	Sequence 5, Appl1
29	10.8	72.0	25	3	US-08-688-514-5	Sequence 5, Appl1
30	10.8	72.0	27	3	US-09-126-280-6	Sequence 6, Appl1
31	10.8	72.0	28	4	US-09-398-217-3	Sequence 3, Appl1
32	10.8	72.0	28	4	US-09-562-331-3	Sequence 3, Appl1
33	10.8	72.0	29	4	US-09-398-217-5	Sequence 5, Appl1
34	10.8	72.0	29	4	US-09-398-217-7	Sequence 7, Appl1
35	10.8	72.0	29	4	US-09-562-331-5	Sequence 5, Appl1
36	10.8	72.0	29	4	US-09-562-331-7	Sequence 7, Appl1
37	10.8	72.0	30	4	US-08-159-106-9	Sequence 9, Appl1
38	10.8	72.0	30	6	US-08-310-416A-8	Patent No. 5187076
39	10.8	72.0	33	1	US-08-888-171-8	Sequence 8, Appl1
40	10.8	72.0	33	2	US-08-840-316-106	Sequence 106, App
41	10.8	72.0	33	3	US-08-809-523-106	Sequence 106, App
42	10.8	72.0	33	4	US-08-471-971-106	Sequence 106, App
43	10.8	72.0	34	1	US-08-458-084-19	Sequence 19, Appl
44	10.8	72.0	34	1	US-08-205-508-19	Sequence 19, Appl
45	10.8	72.0				

ALIGNMENTS

RESULT 1
US-08-465-485A-15
Sequence 15, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-15

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCGGCGACGGA 15
|||||

DB 1 CGCGGCGGCGACGGA 15

RESULT 2
US-09-080-285-15
; Sequence 15, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-15

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCGGCGACGGA 15
|||||

DB 1 CGCGGCGGCGACGGA 15

RESULT 3
US-08-343-443B-46
; Sequence 46, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Auriat, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmarte, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-343-443B-46

Query Match 89.3%; Score 13.4; DB 2; Length 69;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGCGGCGACGGA 15
|||||

DB 45 CGCGGCGGCGACGGA 59

RESULT 4
5262866-3/c
; Patent No. 5262866
; APPLICANT: FRITSCH, EDWARD F.; COLLINS, MARY
; TITLE OF INVENTION: PROCESS AND NUCLEIC ACID CONSTRUCT FOR

PRODUCING REAGENT COMPLEXES USEFUL IN DETERMINING TARGET
NUCLEOTIDE SEQUENCES
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,201
FILING DATE: 11-APR-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 729,504
FILING DATE: 02-MAY-1985
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
APPLICATION NUMBER: 684,308
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 684,305
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
SEQ ID NO: 3:
LENGTH: 17
5262866-3

Query Match 82.7%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgaggcgacgga 15
||||| |||||||
Db 16 GCGCGGTCGACGGA 3

RESULT 5
US-08-519-300-2/c
Sequence 2, Application US/08519300
Patent No. 5834224
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Electrochemical Sensor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,300
FILING DATE: 8/23/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 30 023.9
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: JOHN A. BAUER
REGISTRATION NUMBER: 32,554
REFERENCE/DOCKET NUMBER: HUBR-1070 PFF/JAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: oligonucleotide

US-08-519-300-2

Query Match 78.7%; Score 11.8; DB 2; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcgaggcgacgga 15
||||| |||||||
Db 17 GCGCGGTCGACGGA 3

RESULT 6
US-08-002-024B-11/c
Sequence 11, Application US/08002024B
Patent No. 5798103
GENERAL INFORMATION:
APPLICANT: MOOI, Frederik R
TITLE OF INVENTION: WHOPPING COUGH VACCINE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: US
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,024B
FILING DATE: 08-JAN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200038.5
FILING DATE: 08-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Robert J
REGISTRATION NUMBER: 17,355
REFERENCE/DOCKET NUMBER: BO-37424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/521-2297
TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: YES
US-08-002-024B-11

Query Match 78.7%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcgaggcgacgga 15
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Db 20 GCGCGGTCGACGGA 6

RESULT 7
US-09-450-656-14/c
Sequence 14, Application US/09450656
Patent No. 6251606
GENERAL INFORMATION:
APPLICANT: HSEU, Ruey-Shyang

APPLICANT: CHEN, Chih-Shang
TITLE OF INVENTION: Gene Sequence and Method for Distinguishing Cordyceps sinensis
Patent No. 6251606
FILE REFERENCE: 2410-166P
CURRENT APPLICATION NUMBER: US/09/450,656
CURRENT FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 52
TYPE: DNA
ORGANISM: Cordyceps liangshanensis
US-09-450-656-14

Query Match 78.7%; Score 11.8; DB 4; Length 52;
Best Local Similarity 86.7%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcgggcgacgga 15
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DB 29 GGGCGGGCGCGCGA 15

RESULT 8
US-09-150-900-32
Sequence 32, Application US/09150900
Patent No. 6207425
GENERAL INFORMATION:
APPLICANT: Liu, Oulang
APPLICANT: Sommer, Steve S.
TITLE OF INVENTION: BIDIRECTIONAL PCR AMPLIFICATION OF SPECIFIC ALLELES
FILE REFERENCE: BI-PASA
CURRENT APPLICATION NUMBER: US/09/150,900
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 60/058575
EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-09-150-900-32

Query Match 76.0%; Score 11.4; DB 4; Length 30;
Best Local Similarity 92.3%; Pred. No. 3.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcggggcgacgg 14
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DB 3 ggcggggcgacgg 15

RESULT 9
US-09-499-884-12
Sequence 12, Application US/09499884
Patent No. 6265172
GENERAL INFORMATION:
APPLICANT: St. Clair, Daret
APPLICANT: Urano, Muneyasu
APPLICANT: Kasarskis, Edward
TITLE OF INVENTION: DIAGNOSTIC TEST AND THERAPY FOR MANGANESE SUPEROXIDE DISMUTASE
FILE REFERENCE: 50229-180
CURRENT APPLICATION NUMBER: US/09/499,884
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 38
TYPE: DNA

ORGANISM: Homo sapiens
US-09-499-884-12

Query Match 76.0%; Score 11.4; DB 4; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcggggcgacgg 14
||||| |||
DB 26 ggcggggcgacgg 38

RESULT 10
PCT-US95-10973A-55/C
Sequence 55, Application PC/TUS9510973A
GENERAL INFORMATION:
APPLICANT: Pizim Pharmaceuticals, Inc.
TITLE OF INVENTION: COMBIGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10973A
FILING DATE: 29-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Notenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.413PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
PCT-US95-10973A-55

Query Match 76.0%; Score 11.4; DB 5; Length 41;
Best Local Similarity 92.3%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcggggcgacgg 14
||||| |||
DB 27 GGGCGGGCGCGCGG 15

RESULT 11
US-08-171-389-300
Sequence 300, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-171-389-300

Query Match 76.0%; Score 11.4; DB 1; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 gcggggcgacgga 15
|||||||
Db 31 GCGGGCGCCCGGA 43
RESULT 12
US-08-123-936-300
Sequence 300, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-123-936-300

Query Match 76.0%; Score 11.4; DB 1; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 gcggggcgacgga 15
|||||||
Db 31 GCGGGCGCCCGGA 43
RESULT 13
US-08-475-228A-300
Sequence 300, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: FTY, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-475-228A-300

Query Match 76.0%; Score 11.4; DB 2; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
DB 31 GCGGGGCGCCGGA 43

RESULT 14
US-08-482-080A-300
Sequence 300, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-482-080A-300

Query Match 76.0%; Score 11.4; DB 3; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gcggggcgacgga 15
|||||
DB 31 GCGGGGCGCCGGA 43

RESULT 15
PCT-US93-12388-300
Sequence 300, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783

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; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
; PCT-US93-12388-300

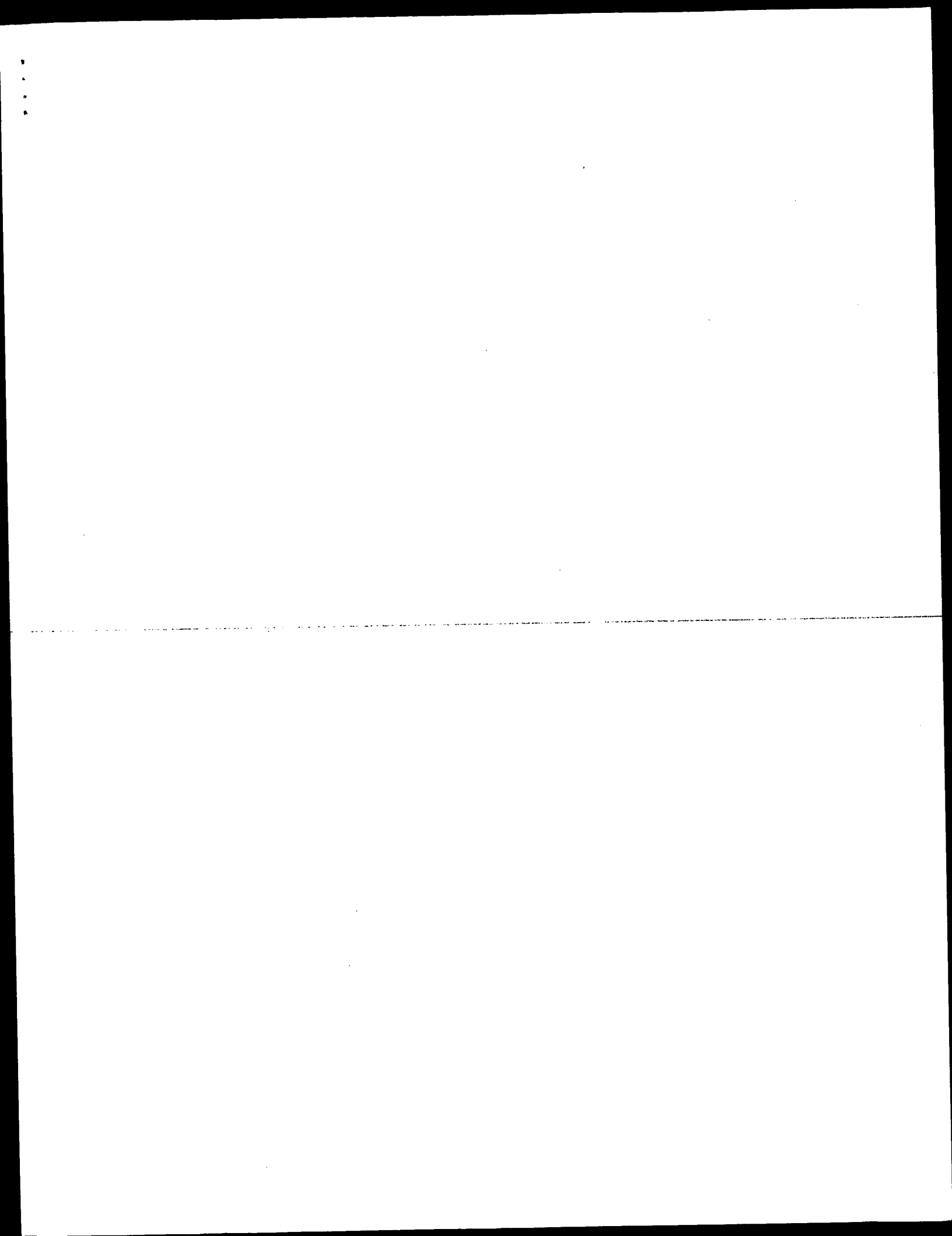
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Query Match          76.0%; Score 11.4; DB 5; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 31 GCGGGGCGCCGGA 43

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-709-170A-15

Sequence: 1 cggcgggggcgacgga 15

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	15	100.0	15	AAV28179	Antisense oligonuc
3	15	100.0	15	AAV23691	Deletion sequence
4	15	100.0	15	AAV18700	Target bcl-2 anti
5	12.4	82.7	29	AAV41907	Nucleotide sequence
6	12.4	82.7	71	AAV35957	5' primer used to
7	12.4	82.7	71	AAV35961	5' primer used to
8	11.8	78.7	24	AA048034	find primer #1. B
9	11.8	78.7	36	AAV52817	Oligonucleotide #1

C	10	11.8	78.7	36	19	AAV52818	Oligonucleotide #2
	11	11.8	78.7	40	21	AAV52327	Cenarchaem symbio
	12	11.8	78.7	40	21	AAV52327	Polynucleotide seq
	13	11.8	78.7	50	22	AAV34175	Human SNP oligonuc
	14	11.8	78.7	51	22	AAH38708	Human SNP flanking
	15	11.8	78.7	52	22	AAH38708	Cordyceps liangsha
	16	11.8	78.7	74	21	AAH16720	Human secreted pro
	17	11.4	76.0	18	24	ABA03344	S chrysomallus act
	18	11.4	76.0	25	22	AAV90232	Genomic walking pr
	19	11.4	76.0	30	22	AAV30580	Human COMT gene PC
	20	11.4	76.0	30	24	ABA03342	Streptomyces chrys
	21	11.4	76.0	38	22	AAH14353	Human manganese su
	22	11.4	76.0	40	22	AAH46088	Synthetic primer 4
	23	11.4	76.0	45	15	AA069550	Human transferrin
	24	11.4	76.0	45	18	AAH64012	Human T-cell recep
	25	11.4	76.0	45	20	AAV17300	Test sequence from
	26	11.4	76.0	47	21	AAH69475	Human map-related
	27	11.4	76.0	51	22	AAH34330	Human SNP oligonuc
	28	11.4	76.0	51	22	AAH90447	Human clone cg4394
	29	11.4	76.0	51	22	AAH90448	Human clone cg4394
	30	11.4	76.0	59	18	AAH73794	Multiplex short-PC
	31	11.4	76.0	70	21	AAH20928	Human FK-506 bindi
	32	11.4	76.0	70	21	AAH34806	Human adenosine re
	33	11.4	76.0	17	23	ABK00033	Human NOGO Hammer
	34	11.4	76.0	17	23	ABK00855	Human NOGO Inozyme
	35	11.4	76.0	17	23	ABK00856	Human NOGO Inozyme
	36	11.4	76.0	17	23	ABK01574	Human NOGO G-Cleav
	37	11.4	76.0	17	23	ABK01817	Human NOGO Kinzyme
	38	11.4	76.0	18	22	AAH26672	Human Sma27 phosph
	39	11.4	76.0	23	11	AAQ03769	Tissue plasminogen
	40	11.4	76.0	29	21	AAH04042	Polymorphic triage
	41	11.4	76.0	30	14	AAQ42711	Sequence of primer
	42	11.4	76.0	46	24	ABA01544	Mycamineose biosynt
	43	11.4	76.0	51	22	AAH27076	Human SNP oligonuc
	44	11.4	76.0	60	22	AAH19843	Synthetic DNA for
	45	10.8	72.0	15	22	AAH70023	Human TFRSFL1B ge

ALIGNMENTS

RESULT	1
ID	AA086657 standard; DNA; 15 BP.
XX	AA086657:
AC	27-SEP-1995 (first entry)
DT	Bcl-2 antisense oligonucleotide.
XX	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	Synthetic.
OS	Key
XX	misc-feature
FT	location/Qualifiers
FT	1..15
FT	/*tag=
FT	/note= "3'-5' (antisense) sequence"
XX	W09508350-A.
XX	30-MAR-1995.
XX	20-SEP-1994; 94WO-US10725.
XX	20-SEP-1993; 93US-0124256.
XX	(REED/) REED J C.
XX	Reed JC;
XX	

DR WPI: 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11845. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ8650-55) or the 5'-cap
CC region (AAQ8656-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 T; 0 other;

Query Match 100.0%; Score 15; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcggggcgacgga 15
1 cggcggggcgacgga 15
Db 1 cggcggggcgacgga 15

RESULT 2
AAV28179
ID AAV28179 standard; DNA; 15 BP.
XX
AC AAV28179;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KM Purification: oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
PI WPI: 1998-362922/31.
XX
DR WPI: 1998-362922/31.
XX
PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 84; 183pp; English.
XX
CC AAV2815-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 15; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcggggcgacgga 15
1 cggcggggcgacgga 15
Db 1 cggcggggcgacgga 15

RESULT 3
AAV23691
ID AAV23691 standard; DNA; 15 BP.
XX
AC AAV23691;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 144.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
PI WPI: 1999-205198/17.
XX
DR WPI: 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 152; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 15;

KM Screening; functional polypeptide; ligand; non-functional;
 KW enrichment; single chain antibody; PCR primer; ss.
 XX
 OS Synthetic.

XX WO9920749-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-GB03135.

XX 21-NOV-1997; 97US-0066729.

XX 20-OCT-1997; 97GB-0022131.

XX 13-NOV-1997; 97US-0065428.

XX (MED-) MEDICAL RES COUNCIL.

XX Tomlinson I, Winter G;

XX WPI; 1999-288302/24.

XX Screening for functional polypeptides which bind a ligand

XX Example 2; Page 50; 67pp; English.

XX The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. PCR primers
 CC AAX35957-58 were used to amplify a germline V gene fragment, which was
 CC used in the construction of libraries of the invention.
 XX
 SQ Sequence 71 BP; 12 A; 17 C; 33 G; 9 T; 0 other;

Query Match 82.7%; Score 12.4; DB 20; Length 71;
 Best Local Similarity 92.9%; Pred. No. 5.7e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ggcgggagcagcga 15
 ||||| |||||
 DB 40 ggcgggagcagcga 53

RESULT 7
 AAX35961
 ID AAX35961 standard; DNA; 71 BP.

XX AAX35961;

XX 15-JUL-1999 (first entry)

XX 5' primer used to amplify germline V gene segment DPK9#.

XX Screening; functional polypeptide; ligand; non-functional;

XX enrichment; single chain antibody; PCR primer; ss.

XX Synthetic.

XX WO9920749-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-GB03135.

PR 21-NOV-1997; 97US-0066729.
 PR 20-OCT-1997; 97GB-0022131.
 PR 13-NOV-1997; 97US-0065428.

XX (MED-) MEDICAL RES COUNCIL.

XX Tomlinson I, Winter G;

XX WPI; 1999-288302/24.

XX Screening for functional polypeptides which bind a ligand

XX Example 2; Page 50; 67pp; English.

XX The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. PCR primers
 CC AAX35960-61 were used to amplify a germline V gene fragment, which was
 CC used in the construction of libraries of the invention.
 XX
 SQ Sequence 71 BP; 12 A; 17 C; 33 G; 9 T; 0 other;

Query Match 82.7%; Score 12.4; DB 20; Length 71;
 Best Local Similarity 92.9%; Pred. No. 5.7e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ggcgggagcagcga 15
 ||||| |||||
 DB 40 ggcgggagcagcga 53

RESULT 8
 AAQ48034/C
 ID AAQ48034 standard; DNA; 24 BP.

XX AAQ48034;

XX 08-FEB-1994 (first entry)

XX fimb primer #1.

XX N-terminal; minor; fimbrial subunit; B. pertussis; fimbriae; fimb;

XX vaccine; whooping cough; immune response; B. parapertussis; PCR;

XX B. bronchiseptica; polymerase chain reaction; primer; amplify; ss.

XX Bordetella pertussis.

XX EP555894-A.

XX 18-AUG-1993.

XX 08-JAN-1993; 93EP-0200047.

XX 08-JAN-1992; 92EP-0200038.

XX (NEME-) NEDERLANDEN MIN WELZIJN.

XX MOOI FR;

XX WPI; 1993-260156/33.

XX Vaccines against whooping cough - contains functional component
 of fimbriae of B. pertussis and can also be used in veterinary

CC (2). The inventions can be used for the production of monoclonal
CC antibodies for medical use which are of human type and therefore not
CC antigenic in humans. They can also be used in the production of chimeric
CC and transgenic animals which express useful foreign proteins, or which
CC can serve as models for the study of human diseases. AAV52755 to
CC AAV52828 are PCR primers used in examples from the present invention.
XX
SQ Sequence 36 BP; 5 A; 12 C; 13 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 19; Length 36;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcgggcgacgca 15
1 | | | | | | | | | |
Db 35 CCGCGGCGTGCACGCA 21

RESULT 11
ID AAA55227 standard; DNA; 40 BP.
XX

AC AAA55227;
XX
DT 30-AUG-2000 (first entry)
XX

DE Cenarchaeum symbiosum promoter nucleotide sequence SMO ID NO:81.
XX

KW Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology;
KW characterisation; archae; therapeutic; industrial; laboratory;
KW promoter; ds.
XX

OS Cenarchaeum symbiosum.
XX

PN WO200018909-A2.
XX

PD 06-APR-2000.
XX

PF 29-SEP-1999; 99WO-US22752.
XX

PR 29-SEP-1998; 98US-0102294.
XX

PA (DIVE-) DIVERSA CORP.
XX

PI Swanson RV, Feldman RA, Schleper C;
XX

DR WPI; 2000-293148/25.
XX

PT New nucleic acids and proteins isolated from the non-thermophilic
PT crenarchaeote Cenarchaeum symbiosum, useful in characterizing the
PT physiology of these archae and in therapeutic, industrial or laboratory
PT techniques -
XX

PS Example 8; Page 201; 210pp; English.
XX

CC AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acids
CC and proteins isolated from the non-thermophilic crenarchaeote
CC Cenarchaeum symbiosum. The nucleic acids and proteins identified in
CC the present invention are useful in characterizing the physiology of
CC these archae and can be used in therapeutic, industrial or laboratory
CC techniques. AAA55227 to AAA55260 represent promoter sequences from
CC Cenarchaeum symbiosum. AAA55261 to AAA55269 represent PCR primers and
CC probes used in examples from the present invention.
XX

SQ Sequence 40 BP; 8 A; 8 C; 15 G; 9 T; 0 other;

Query Match 78.7%; Score 11.8; DB 21; Length 40;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcgggcgacgca 15

Db 24 cggcgggcgacgca 38
| | | | | | | | | |

RESULT 12
ID AA295998 standard; DNA; 40 BP.
XX

AC AA295998;
XX

DT 10-APR-2000 (first entry)
XX

DE Polynucleotide sequence including binding site for BamHI.
XX

KW Ligand binding; restriction enzyme; nucleic acid determination;
KW pharmaceutical; BamHI; ss.
XX

OS Synthetic.
XX

PN WO963077-A2.
XX

PD 09-DEC-1999.
XX

PF 04-JUN-1999; 99WO-US12516.
XX

PR 04-JUN-1998; 98US-0087905.
XX

PR 03-JUN-1999; 99US-0324672.
XX

PA (TME-) TM TECHNOLOGIES INC.
XX

PI Lane MJ, Benight AS, Faldasz BD;
XX

DR WPI; 2000-116369/10.
XX

PT Modulating polynucleotide ligand binding site affinity using
PT determination of the flanking duplex sequences -
XX

PS Example 1; Page 41; 62pp; English.
XX

CC The invention provides a method for determining the sequence of
CC polynucleotide flanking regions that modulate ligand binding
CC characteristics of an adjacent binding site. The method comprises:
CC (i) providing a number of different duplex polynucleotides, each having
CC the same polynucleotide ligand binding site and a randomly synthesised
CC sequence flanking the binding site; (ii) exposing the duplex to a ligand
CC selective for the binding site; (iii) isolating the duplex to a ligand
CC do not bind the ligand, and (iv) determining the nucleotide composition
CC of the flanking duplex sequence by sequencing the duplex sequence
CC adjacent to the binding site. The invention is used to modulate the
CC ligand-binding characteristics of any nucleotide sequence. The invention
CC is less costly and more efficient than prior art techniques that moderate
CC ligand binding using small molecule pharmaceuticals. Sequences
CC AA295762-296170 represent polynucleotide sequences including the binding
CC site for the restriction enzyme BamHI and used in the course of the
CC invention.
XX

SQ Sequence 40 BP; 3 A; 10 C; 21 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 21; Length 40;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcgggcgacgca 15
1 | | | | | | | | | |
Db 22 cggcgggcgacgca 36

RESULT 13
ID AAL34175/C standard; DNA; 50 BP.
XX

AC AAL34175;
XX

Human SNP flanking oligonucleotide SEQ ID 1504.

Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia
polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
inflammation; forensic investigation; paternity analysis; ds.
OS
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000MO-US28436.
XX
XX PR 15-OCT-1999; 99US-0160096.
XX
XX (ORCH) ORCHID BIOSCIENCES INC.
XX
XX PI Picoult-Newburg L, Fohl M;
XX
XX DR WPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
XX PS Claim 1; Page 57; 83pp; English.
XX

Sequences AAH37205 - AAH4094 represent PCR primers, single nucleotide
primer extension (SNPE) primers, and the sequences of regions flanking
sites of single nucleotide polymorphisms SNPs. The present invention
includes kits for determining the presence or absence of a SNP, using the
oligonucleotides of the invention. The PCR primers are used to amplify a
SNP flanking sequence, the SNPE primer is used as a genotyping primer.
The oligonucleotides are useful for genotyping a nucleic acid sample by
performing a single-nucleotide primer extension reaction. The
oligonucleotides are useful for determining the presence, absence or
identity of a SNP and for genotyping nucleic acid samples, for e.g. to
assess by association analysis the genotype of an individual or group of
individuals, having a pathological phenotypic trait suspected of being
caused by one or more SNPs. Phenotypic traits include diseases e.g.
agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
traits also include symptoms of or susceptibility to multifactorial
disease of which a component is or may be genetic such as autoimmune
diseases, including, rheumatoid arthritis, multiple sclerosis,
microangioma, cancer, nervous system diseases and infection by pathogenic
inflammation. The method is also useful in forensic investigations and
DNA flanking the site of a single nucleotide polymorphism.

Sequence 51 BP; 8 A; 25 C; 5 G; 13 T; 0 other:

Query Match 78.7%; Score 11.8; DB 22; Length 51;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGCGGAGGCACAGA 15
|||||||
Db 20 CGGCGGAGCAGACGA 6

RESULT 15
AAAS08614/C
ID AAAS08614 standard; DNA; 52 BP.
XX

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:10 ; Search time 1381.16 Seconds

(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-7

Perfect score: 20

Sequence: 1 g9gaagcagcgcacgctg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	16	AA086649	Bcl-2 translation
2	20	100.0	20	19	AAV19651	Human bcl-2 antisense
3	20	100.0	20	19	AAV19657	Human bcl-2 transcr
4	20	100.0	20	22	AAV15276	Human bcl-2 mRNA t
5	20	100.0	20	22	AAV12300	AM-TIS sulphate-ol
6	20	100.0	20	22	AAV12301	Bcl-2-TIS sulphate
7	20	100.0	20	22	AAV77808	Bcl-2 antisense ol
8	20	100.0	20	22	AAV77809	Control sense olig
9	20	100.0	22	14	AA049816	Bcl-2 antisense ol

C	10	20	100.0	22	14	AA049817	Bcl-2 antisense ol
C	11	20	100.0	35	16	AA086644	Bcl-2 translation
C	12	20	100.0	35	19	AAV19652	Human bcl-2 oligon
C	13	19	95.0	20	22	AAV19657	Human bcl-2 xl and b
C	14	18	90.0	18	19	AAV11591	Liposomal bcl-2 an
C	15	17.6	88.0	21	21	AAV1591	Human bcl genes an
C	16	17	85.0	17	19	AAV19661	Human bcl-2 antis
C	17	17	85.0	19	20	AAV06730	Antisense oligomer
C	18	16	80.0	17	19	AAV19660	Human bcl-2 antis
C	19	15.8	79.0	51	23	ABL00944	Human amino acid c
C	20	15	75.0	15	22	AAV15281	Human bcl-2 mRNA t
C	21	15	75.0	15	22	AAV15282	Human bcl-2 mRNA t
C	22	15	75.0	17	19	AAV19662	Human bcl-2 antis
C	23	14	70.0	36	22	AAV45307	Human bcl-2 PCR pr
C	24	13.8	69.0	50	22	AAV45316	PCR primer used to
C	25	13.8	69.0	60	22	AAV45317	PCR primer used to
C	26	13.6	69.0	70	22	AAV45318	PCR primer used to
C	27	13.6	68.0	27	17	AAV18338	Human bcl-2 forwar
C	28	13.6	68.0	70	21	AAV11411	Human secreted pro
C	29	13.4	67.0	24	24	AAV18324	Capture oligonucle
C	30	13.4	67.0	24	24	AAV18325	Capture oligonucle
C	31	13.2	66.0	47	17	AAV28357	HCV primer used in
C	32	13.2	66.0	47	17	AAV28359	HCV primer used in
C	33	13.2	66.0	51	21	AAV76662	Human clone c92784
C	34	13.2	66.0	51	21	AAV76663	Human clone c92784
C	35	13.2	66.0	51	21	AAV76664	Human clone c92784
C	36	13.2	66.0	51	21	AAV76665	Human clone c92784
C	37	13.2	66.0	51	22	AAV74164	Human silent SNP c
C	38	13.2	66.0	51	22	AAV74165	Human silent SNP c
C	39	13.2	66.0	51	23	AAV00223	Human silent nonco
C	40	13	65.0	16	22	AAV98965	Immunostimulatory
C	41	13	65.0	17	19	AAV19659	Human bcl-2 antis
C	42	13	65.0	18	16	AA086659	Bcl-2 antisense ol
C	43	13	65.0	18	19	AAV52545	Unmethylated CpG d
C	44	13	65.0	18	19	AAV27719	Immunostimulatory
C	45	13	65.0	18	19	AAV28181	Antisense oligonuc

ALIGNMENTS

RESULT 1

AA086649

ID AA086649 standard; DNA; 20 BP.

AC AA086649;

XX

XX 27-SEP-1995 (first entry)

XX

DE Bcl-2 translation initiation site region.

XX

XX

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss.

XX

XX

OS Synthetic.

OS

PN W09508350-A.

PD 30-MAR-1995.

XX

XX 20-SEP-1994; 94WO-US10725.

PF

XX 20-SEP-1993; 93US-0124256.

PR

XX

XX (REED/) REED J C.

XX

XX

XX Reed JC;

XX

XX WPI; 1995-139394/18.

DR

XX

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

XX

PS Example 12; Page 33; 108bp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086650-55) or the 5'-cap
CC region (AA086656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
CC (AA086649) was used as a control.
XX
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagagatgagcagcagctg 20
1 ggaagagatgagcagcagctg 20
Db 1 ggaagagatgagcagcagctg 20

RESULT 2
AAV19651/c
ID AAV19651 standard; DNA; 20 BP.
XX
XX AAV19651;
AC
XX
XX 12-JUN-1998 (first entry)
DT
XX
XX Human bcl-2 antisense oligonucleotide 1.
DE
XX
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX
XX US5734033-A.
PN
XX
XX 31-MAR-1998.
PD
XX
XX 24-MAR-1994; 94US-0288692.
PF
XX
XX 21-FEB-1992; 92US-0840716.
PR
XX 22-DEC-1988; 88US-0288692.
PR
XX 24-MAR-1994; 94US-0217082.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Reed J;
PI
XX
XX WPI; 1998-229881/20.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
XX
XX
PS Claim 6; Columns 3-4; 21pp; English.
XX
XX This antisense oligonucleotide is complementary to the translation
XX initiation site of the human bcl-2 mRNA. The bcl-2 antisense
XX oligonucleotides are phosphorothioate derivatives and can straddle
XX strategic sites such as the translation initiation site, donor and
XX acceptor splicing sites, or sites for transportation or degradation.
XX Blocking translation at such strategic sites prevents the formation of
XX a functional bcl-2 gene product. These oligonucleotides may be used for
XX treating cancers associated with high levels of bcl-2 gene expression,
XX especially lymphomas and some leukaemias.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagagatgagcagcagctg 20
1 ggaagagatgagcagcagctg 20
Db 20 GGGAAGATGGCGCACGCTG 1

RESULT 3
AAV19657
ID AAV19657 standard; DNA; 20 BP.
XX
XX AAV19657;
AC
XX
XX 12-JUN-1998 (first entry)
DT
XX
XX Human bcl-2 transcription initiation sense (TI-S) oligonucleotide.
DE
XX
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX
XX US5734033-A.
PN
XX
XX 31-MAR-1998.
PD
XX
XX 24-MAR-1994; 94US-0288692.
PF
XX
XX 21-FEB-1992; 92US-0840716.
PR
XX 22-DEC-1988; 88US-0288692.
PR
XX 24-MAR-1994; 94US-0217082.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Reed J;
PI
XX
XX WPI; 1998-229881/20.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
XX
XX
PS Disclosure; Column 19; 21pp; English.
XX
XX This oligonucleotide is used as a control in measuring DNA fragmentation
XX as an indicator of bcl-2 antisense oligonucleotide mediated programmed
XX cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
XX straddle strategic sites such as the translation initiation site, donor
XX and acceptor splicing sites, or sites for transportation or degradation.
XX Blocking translation at such strategic sites prevents the formation of a
XX functional bcl-2 gene product. These oligonucleotides may be used for
XX treating cancers associated with high levels of bcl-2 gene expression,
XX especially lymphomas and some leukaemias.
XX
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagagatgagcagcagctg 20
1 ggaagagatgagcagcagctg 20
Db 1 ggaagagatgagcagcagctg 20

RESULT 4
AAD15276/c
ID AAD15276 standard; DNA; 20 BP.
XX
XX AAD15276;
AC
XX
XX 15-NOV-2001 (first entry)
DT


```
XX Human Bcl-2 mRNA targeted liposomal antisense oligonucleotide #1.
DE
XX
XX
KW Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; antisense;
KW chronic lymphocytic leukaemia; plasma cell dyscrasia; cancer; pancreas;
KW breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
KW testes; skin; head; kidney; colon; immune disorder; liposome; ss.
XX
XX Homo sapiens.
XX
XX WO200160998-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US40159.
XX
XX 18-FEB-2000; 2000US-0506979.
XX
XX (TEXA ) UNTV TEXAS SYSTEM.
XX
XX Tarr AM, Lopez-Berestein G, Gutierrez-Puente Y;
XX WPI; 2001-529911/58.
XX
XX Compositions comprising short antisense oligonucleotides and a lipid
XX component, useful for treating Bcl-associated diseases, e.g. cancer -
XX
XX Example 1; Page 31; 63pp; English.
XX
XX The invention relates to a liposomal composition of antisense
XX oligonucleotides targeted to the translation initiation site of human
XX Bcl-2 mRNA. The invention also relates to a method useful for treating
XX Bcl-associated diseases like cancer such as follicular and nonfollicular
XX lymphomas, chronic lymphocytic leukaemia and plasma cell dyscrasias;
XX solid tumours like those associated with breast, prostate, liver,
XX pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
XX stomach, kidney and colon cancer; and immune disorders. The present DNA
XX sequence is liposomal antisense oligonucleotide targeted to the
XX translation initiation site of human Bcl-2 mRNA. This antisense
XX oligonucleotide which is preferably composed of a nuclease resistant
XX backbone is able to inhibit the production of Bcl-2 protein.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;
XX
SQ
Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gggaaggatgagcgcacgctg 20
Db 20 GGGAAGGATGCGCGACGCTG 1
RESULT 5
AADI2300
ID AADI2300 standard; DNA; 20 BP.
XX
XX AADI2300;
XX
XX 06-NOV-2001 (first entry)
XX
DE AM-TIS sulphate-oligonucleotide to detect binding of charged species.
XX
XX AM-TIS sulphate-oligonucleotide; DNA transfection; fluorophore;
KW biomolecule; charged species; lipid vesicle; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX FT 1 /*tag=
XX FT /mod_base= OTHER
XX
```

```
FT /note="Optionally labelled with FIRC
FT (fluoresceinisothiocyanate)"
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="Sulphate-oligodeoxynucleotide"
XX
XX WO200159156-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-IL00134.
XX
XX 10-FEB-2000; 2000US-0181693.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Barenholz Y, Hirsch-Jerner D, Cohen R, Dagan A, Gatt S;
XX WPI; 2001-497084/54.
XX
XX Determining binding of compounds to a surface, particularly of DNA to
XX transfection vesicle, using lipid-coupled fluorophore as pH- or
XX potential-sensitive probe -
XX
XX Example 4; Page 20; 39pp; English.
XX
XX The invention relates to a method for determining the binding of a
XX species at a surface, where binding alters the local pH or the surface
XX potential, by stable incorporation of a probe at the surface. Probe
XX consists of a pH- or potential-sensitive fluorophore attached to either
XX a steroid or a lipid having at least two alkyl or alkenyl chains of at
XX least 14 carbons. A change in fluorescence from fluorophore when a
XX species binds to, or is released from, the surface is detected.
XX The method is used for determining the extent of binding of species,
XX particularly a biomolecule (nucleic acid or protein) to a surface or its
XX release from the surface. Particularly the surface is a lipid vesicle
XX being used for DNA transfection or a cell membrane. The method is also
XX useful for monitoring transfection of DNA to cells, in vivo or in vitro.
XX The method is used for detecting both specific and non-specific
XX interactions at the surface. The lipid/steroid component ensures stable
XX incorporation of the probe, thus stable and reproducible observation of
XX interactions. The present DNA sequence is an AM-TIS sulphate-
XX oligodeoxynucleotide which is used to detect the binding of charged
XX species.
XX
XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
XX
SQ
Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gggaaggatgagcgcacgctg 20
Db 1 gggaaggatgagcgcacgctg 20
RESULT 6
AADI2301/c
ID AADI2301 standard; DNA; 20 BP.
XX
XX AADI2301;
XX
XX 06-NOV-2001 (first entry)
XX
DE Bcl2-TIAS sulphate-oligonucleotide to detect binding of charged species.
XX
XX Bcl2-TIAS sulphate-oligonucleotide; DNA transfection; fluorophore;
KW biomolecule; charged species; lipid vesicle; ss.
XX
XX Unidentified.
XX
XX
```


DR WPI: 2001-257588/26.

XX Delivering antisense oligodeoxynucleotide to cells for treating
PT cancers, involves forming a complex comprising the oligodeoxynucleotide
PT and a polynuclear platinum compound, and providing the complex to the
PT cells

PS Example 4; Page 28; 52pp; English.

XX The present invention relates to a method for delivering an antisense
CC oligodeoxynucleotide to cells. The method comprises forming a complex
CC comprising the antisense oligonucleotide and a polynuclear platinum
CC compound, and providing the complex to the cells. The present sequence is
CC a control sense oligonucleotide which was used in an assay for Bcl-2
CC antisense oligonucleotide activity (see AAF7808). Bcl-2 is a suppressor
CC of apoptosis and its expression in cancer cells may contribute to the
CC resistance of cancer cells to apoptosis. The complex of the present
CC invention is useful for treating cancer and any other disease amenable to
CC the treatment by antisense oligonucleotides.

XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

SO

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggaagatgagcgcacgctg 20
|||||
DB 1 gggaagatgagcgcacgctg 20

RESULT 9
AAQ49816/C
ID AAQ49816 standard; DNA; 22 BP.

XX AAQ49816;
AC
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX WO9320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PE
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX 02-APR-1992; 92GB-0007276.
PS
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing Bcl-2
XX
XX
PS Disclosure; Page 58; 109pp; English.

XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.

CC of bcl-2 antisense oligonucleotides.

XX

SO Sequence 22 BP; 2 A; 12 C; 4 G; 4 T; 0 other;

XX

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggaagatgagcgcacgctg 20
|||||
DB 22 GGGAAGATGAGCGCACGCTG 3

RESULT 10
AAQ49817/C
ID AAQ49817 standard; RNA; 22 BP.

XX AAQ49817;
AC
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX WO9320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PE
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX 02-APR-1992; 92GB-0007276.
PS
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing Bcl-2
XX
XX
PS Disclosure; Page 58; 109pp; English.

XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.

XX Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;

SO

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggaagatgagcgcacgctg 20
|||||
DB 22 GGGAAGATGAGCGCACGCTG 3

RESULT 11
AAQ86644
ID AAQ86644 standard; DNA; 35 BP.

AC AA086644;
 XX
 DT 27-SEP-1995 (first entry)
 XX
 DE Bcl-2 translation initiation region.
 XX
 KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN W09508350-A.
 XX
 PD 30-MAR-1995.
 XX
 PF 20-SEP-1994; 94WO-US10725.
 XX
 PR 20-SEP-1993; 93US-0124256.
 XX
 PA (REED/) REED J C.
 XX
 PI Reed JC;
 XX
 DR WPI; 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Disclosure; Page 13; 108pp; English.
 XX
 CC The antisense oligonucleotide TI-AS (AA086643) straddles the
 CC translation-initiation site in the mRNA coding strand of the human
 CC bcl-2 gene and is complementary to this region. It reduces the
 CC expression of bcl-2 gene product thereby inducing programmed cell
 CC death of certain cancer cells. The corresp. sense bcl-1 sequence
 CC was synthesized for use as a control.
 XX
 SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;
 XX

Query Match 100.0%; Score 20; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcgacgctg 20
 |||||
 Db 11 gggaagatgagcgacgctg 30

RESULT 12
 AAV19652
 ID AAV19652 standard; DNA; 35 BP.
 XX
 AC AAV19652;
 XX
 DT 12-JUN-1998 (first entry)
 XX
 DE Human bcl-2 oligonucleotide 1.
 XX
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukemia; human;
 KW cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 PF 24-MAR-1994; 94US-0288692.
 XX
 PR 21-FEB-1992; 92US-0840716.
 XX

PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed J;
 XX
 DR WPI; 1998-229881/20.
 XX
 PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 PS Claim 1; Columns 3-4; 21pp; English.
 XX
 CC This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the translation initiation site of the
 CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
 CC straddle strategic sites such as the translation initiation site, donor
 CC and acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 XX
 SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;
 XX

Query Match 100.0%; Score 20; DB 19; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcgacgctg 20
 |||||
 Db 11 gggaagatgagcgacgctg 30

RESULT 13
 AAC86407/C
 ID AAC86407 standard; RNA; 20 BP.
 XX
 AC AAC86407;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human bcl-xl and bcl-2 mRNA antisense control sequence C02.
 XX
 KW Human; bcl-xl; bcl-2; apoptosis; antisense; cancer; allergic disease;
 KW restenosis; fibrosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200066724-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-EP03708.
 XX
 PR 30-APR-1999; 99GB-0010119.
 XX
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Zangemeister-Wittke U, Luedke G, Huesken D;
 XX
 DR WPI; 2001-015981/02.
 XX
 PT Antisense oligonucleotide derivatives directed against human bcl-xl,
 PT mRNA and capable of modulating biosynthesis of human bcl-xl proteins,
 PT useful in treatment and diagnosis of hyperproliferative diseases -
 XX
 PS Example 2; Page 23; 38pp; English.
 XX
 CC The present invention provides antisense nucleotides which hybridise to
 CC the human bcl-xl and bcl-2 mRNA sequences. The bcl-xl and bcl-2 proteins

CC are involved in apoptosis, and the antisense strands can be used to
CC inhibit them and possibly lead to cell death. The nucleic acids of the
CC invention can be used in the treatment of cancer, particularly
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
CC types of allergic disease.

XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 95.0%; Score 19; DB 22; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ggaagatgagcgacgctg 20
DB 20 GGAAGATGAGCGCACGCTG 2

RESULT 14

AAV1591/c
ID AAV1591 standard; DNA; 18 BP.

XX AAV1591;

DT 30-JUL-1998 (first entry)

DE Lipoosomal bcl-2 antisense polynucleotide.

XX Bcl-2; antisense; disease; treatment; cancer; follicular lymphoma;
KW leukaemia; plasma cell dyscrasia; breast; prostate; colon;
XX autoimmune diseases; ss.

OS Synthetic.

OS Homo sapiens.

XX WC9814172-A1.

XX 09-APR-1998.

PF 03-OCT-1997; 97WO-US18348.

PR 04-OCT-1996; 96US-0726211.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Loper-Berestein G, McDonnell TJ, Tara AM, Tormo M;

PI WPI; 1998-239841/21.

DR Composition comprising oligo:nucleotide anti-sense to Bcl-2 gene -
XX useful for, e.g. treatment of Bcl-2 related disease such as

XX follicular lymphoma and auto-immune disease

PS Claim 4; Page 30; 69pp; English.

CC This sequence is a nuclease-resistant p-ethoxy antisense oligonucleotide
CC which specifically binds to the translation initiation site of human
CC Bcl-2 mRNA. This oligonucleotide can be used in a method to treat Bcl-2
CC related disease in humans and animals, e.g. cancer especially follicular
CC lymphoma (FL), leukaemia, plasma cell dyscrasia, cancer of breast,
CC prostate and colon, or autoimmune diseases.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 90.0%; Score 18; DB 19; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 gaagatgagcgacgctg 20
DB 18 GAAGATGAGCGCACGCTG 1

RESULT 15

AAc65064/c
ID AAc65064 standard; DNA; 21 BP.

XX AAc65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

XX Antisense oligonucleotide; RNA molecule cleavage; immune activation;
KW bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

XX WO200061810-A1.

XX 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

XX (OAST-) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal
PT bases, and modified backbone linkages is useful to target therapeutic
XX genes, preferably anti-apoptosis or chemoresistance genes

XX Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
CC containing a number of degenerate bases and with a modified backbone
CC which can be used to direct cleavage of target RNA molecules. The use of
CC degenerate bases reduces the risk of immune activation following
CC injection into animals, which causes deleterious side effects associated
CC with many therapeutic antisense oligonucleotides. Sequences
CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
XX assays to demonstrate the effects of the sequences of the invention.

XX Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match

Best Local Similarity 88.0%; Score 17.6; DB 21; Length 21;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ggaagatgagcgacgctg 20
DB 21 GGAARNATGGCGCACGCTG 3

Search completed: June 28, 2002, 22:40:10
Job time: 8086 sec

Mon Jul 1 08:40:58 2002

us-09-709-170a-7.sz1m75.rng

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 19:51:49 ; Search time 3762.88 Seconds
(without alignments)
111.226 Million cell updates/sec

Title: US-09-709-170A-1
Perfect score: 20
Sequence: 1 cagcgtgcgcacccctccc 20

Scoring table:
IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	gb_hlg:*
3:	gb_in:*
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11:	gb_sy:*
12:	gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	20	100.0	20	6	AR052603	AR052603 Sequence
2	20	100.0	20	6	AR052609	AR052609 Sequence
3	20	100.0	20	6	AR176022	AR176022 Sequence
4	20	100.0	20	6	AR176023	AR176023 Sequence
5	20	100.0	20	6	AX211669	AX211669 Sequence
6	20	100.0	20	6	AX211670	AX211670 Sequence
7	20	100.0	20	6	AX277461	AX277461 Sequence
8	20	100.0	20	6	AX277461	AX277461 Sequence
9	20	100.0	20	6	196082	196082 Sequence 1
10	20	100.0	20	6	196088	196088 Sequence 7
11	20	100.0	22	6	A76123	A76123 Sequence 3
12	20	100.0	22	6	A76124	A76124 Sequence 4
13	20	100.0	35	6	AR052604	AR052604 Sequence 2
14	20	100.0	35	6	196083	196083 Sequence 2
15	19	95.0	20	6	AX045387	AX045387 Sequence
16	18	90.0	18	6	BD008994	BD008994 Inhibitor
17	17	85.0	17	6	196092	196092 Sequence 11
18	16	80.0	17	6	196091	196091 Sequence 10
19	15.8	79.0	51	6	AX165740	AX165740 Sequence
20	15.4	77.0	29	5	CHRC2A101	K02260 Chicken alp
21	15	75.0	15	6	AX277468	AX277468 Sequence
22	15	75.0	15	6	AX277469	AX277469 Sequence
23	14	70.0	19	6	AX083694	AX083694 Sequence 12
24	13.8	69.0	50	6	AX133707	AX133707 Sequence
25	13.8	69.0	60	6	AX113708	AX113708 Sequence
26	13.8	69.0	70	6	AX113709	AX113709 Sequence
27	13.6	68.0	27	6	AR004426	AR004426 Sequence
28	13.6	68.0	27	6	143661	143661 Sequence 13
29	13.6	68.0	27	6	186720	186720 Sequence 8
30	13.4	67.0	24	6	AX290202	AX290202 Sequence
31	13.2	66.0	47	6	AR153764	AR153764 Sequence
32	13.2	66.0	47	6	AR153766	AR153766 Sequence
33	13.2	66.0	51	6	AX157777	AX157777 Sequence
34	13.2	66.0	51	6	AX157778	AX157778 Sequence
35	13.2	66.0	51	6	AX157779	AX157779 Sequence
36	13	65.0	16	6	AX103898	AX103898 Sequence
37	13	65.0	17	6	AX355505	AX355505 Sequence
38	13	65.0	17	6	196090	196090 Sequence 9
39	13	65.0	18	6	AR052619	AR052619 Sequence
40	13	65.0	18	6	AR052624	AR052624 Sequence
41	13	65.0	18	6	AR116926	AR116926 Sequence
42	13	65.0	18	6	AR140496	AR140496 Sequence
43	13	65.0	18	6	AR146347	AR146347 Sequence
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ALIGNMENTS

RESULT 1

AR052603	AR052603	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1 from patent US 5831066.				
DEFINITION	AR052603				
ACCESSION	AR052603.1				
VERSION	GI:5975967				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Reed, J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A1 03-NOV-1998;				
FEATURES	Location/Qualifiers				
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BASE COUNT	2 a 10 c 4 g 4 t				
ORIGIN	./organism="unknown"				

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AR052609/c AR052609 20 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 7 from patent US 5831066.
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES
source location/Qualifiers
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BASE COUNT 4 a 4 c 10 g 2 t
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Best Local Similarity 100.0%; Pred. No. 50;
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RESULT 3
AR176022 AR176022 20 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES
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BASE COUNT 2 a 10 c 4 g 4 t
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAGCGTGCACCATCTCTCCC 20

RESULT 4
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LOCUS
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023

VERSION AR176023.1 GI:17917322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES
source location/Qualifiers
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BASE COUNT 4 a 4 c 10 g 2 t
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 CAGCGTGCACCATCTCTCCC 1

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AX211669/c AX211669 20 bp DNA linear PAT 06-SEP-2001
LOCUS
DEFINITION Sequence 1 from Patent W00159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatl,S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem (IL)

FEATURES
source location/Qualifiers
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/db_xref="taxon:32630"
/note="."

BASE COUNT 4 a 10 g 2 t

QY 1 cagcgtgcgcacatctctccc 20
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Db 20 CAGCGTGCACCATCTCTCCC 1

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LOCUS
DEFINITION Sequence 2 from Patent W00159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatl,S.

TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 2 16-AUG-2001;
Yissum Research Development Co., The Hebrew University of Jerusalem (IL)

FEATURES
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BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Db 1 CAGCGTGGCCATCCTTCCC 20

RESULT 7
AX277461 20 bp DNA PAT 29-OCT-2001
LOCUS AX277461
DEFINITION Sequence 1 from Patent WO0160998.
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Tari, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
TITLE Small oligonucleotides with anti-tumor activity
JOURNAL Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAGCGTGGCCATCCTTCCC 20

RESULT 8
196082 20 bp DNA PAT 01-DEC-1998
LOCUS 196082
DEFINITION Sequence 1 from patent US 5734033.
ACCESSION 196082
VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
FEATURES
source 1. .20
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BASE COUNT 2 a 10 c 4 g 4 t
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Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccacatccttccc 20
|||||
Db 1 CAGCGTGGCCATCCTTCCC 20

RESULT 9
196088/c 20 bp DNA PAT 01-DEC-1998
LOCUS 196088
DEFINITION Sequence 7 from patent US 5734033.
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
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Db 20 CAGCGTGGCCATCCTTCCC 1

RESULT 10
A76123 22 bp DNA PAT 19-OCT-1999
LOCUS A76123
DEFINITION Sequence 3 from Patent WO9320200.
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 3 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccacatccttccc 20
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Db 3 CAGCGTGGCCATCCTTCCC 22

RESULT 11
LOCUS A76124 22 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 4 from Patent WO9320200.
ACCESSION A76124
VERSION A76124.1 GI:6088260
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ewan,G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
IMP CANCER RES TECH (GB); EWAN GERARD IAN (GB)
FEATURES
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BASE COUNT 2 a 12 c 4 g 4 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
LOCUS AR052604 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5831066.
ACCESSION AR052604
VERSION AR052604.1 GI:5975968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;
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BASE COUNT 6 a 8 c 13 g 8 t
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 30 CAGCGTGGCCATCCTTCCC 11

RESULT 13
LOCUS 196083 35 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 2 from patent US 5734033.
ACCESSION 196083
VERSION 196083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
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BASE COUNT 6 a 8 c 13 g 8 t
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcctccc 20
|||||
Db 30 CAGCGTGGCCATCCTTCCC 11

RESULT 14
LOCUS AX045387 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 7 from Patent WO0066724.
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zangemeister-Witke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mna
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense"
BASE COUNT 2 a 10 c 4 g 4 t
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CAGCGTGGCCATCCTTCCC 20

RESULT 15
LOCUS BD008994 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibition of Bcl-2 protein expression by liposomal antisense oligodeoxynucleotides.
ACCESSION BD008994
VERSION BD008994.1 GI:18637367
KEYWORDS JP 2001502172-A/I.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Torno,M., Tara,A.M., Berestrein,G.L. and McDonnell,T.J.
TITLE Inhibition of Bcl-2 protein expression by liposomal antisense oligodeoxynucleotides
JOURNAL Patent: JP 2001502172-A 1 20-FEB-2001;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
COMMENT OS Unidentified

PN JP 2001502172-A/1
 PD 20-FEB-2001
 PF 03-OCT-1997 JP 1998516985
 PR 04-OCT-1996 US 08/726211
 PI MAR TORMO, ANA M TARA, GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
 MCDONNELL
 PC A61K9/127, A61K31/70, C07H21/04, C12N15/00
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 CC Topology: Linear;
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 ORIGIN

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Search completed: June 28, 2002, 22:10:44
 Job time: 8335 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 20:25:24 ; Search time 1381.16 Seconds

(Without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-1

Perfect score: 20
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Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	20	100.0	20	22	AAV15276
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7	20	100.0	20	22	AAV17808
8	20	100.0	20	22	AAV17809
9	20	100.0	22	14	AAQ49816

10	20	100.0	22	14	AAQ49817	Bcl-2 antisense ol
11	20	100.0	35	16	AAQ86644	Bcl-2 translation
12	20	100.0	35	19	AAV19652	Human bcl-2 oligon
13	19	95.0	20	22	AAQ86407	Human bcl-xl and b
14	18	90.0	18	19	AAV11591	Liposomal bcl-2 an
15	17.6	88.0	21	21	AAQ65064	Human bcl genes an
16	17	85.0	17	19	AAV19661	Human bcl-2 antis
17	17	85.0	19	20	AAZ06730	Antisense oligomer
18	16	80.0	17	19	AAV19660	Human bcl-2 antis
19	15.8	79.0	51	23	ABL00944	Human amino acid c
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21	15	75.0	15	22	AAV15282	Human Bcl-2 mRNA t
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23	14	70.0	36	22	AAH45307	Human bcl-2 PCR pr
24	13.8	69.0	50	22	AAV84516	PCR primer used to
25	13.8	69.0	60	22	AAV84517	PCR primer used to
26	13.8	69.0	70	22	AAV84518	PCR primer used to
27	13.6	68.0	27	17	AAV18388	Human Bcl-2 forwar
28	13.6	68.0	70	21	AAV18388	Human secreted pro
29	13.4	67.0	24	24	AAV18388	Human secreted pro
30	13.4	67.0	24	24	AAV18388	Capture oligonucle
31	13.2	66.0	47	17	AAV28357	HCY primer used in
32	13.2	66.0	47	17	AAV28359	HCY primer used in
33	13.2	66.0	51	21	AAV6662	Human clone c92784
34	13.2	66.0	51	21	AAV6663	Human clone c92784
35	13.2	66.0	51	21	AAV6664	Human clone c92784
36	13.2	66.0	51	21	AAV6665	Human clone c92784
37	13.2	66.0	51	22	AAV74164	Human silent SNP c
38	13.2	66.0	51	22	AAV74165	Human silent SNP c
39	13.2	66.0	51	22	AAV74165	Human silent SNP c
40	13	65.0	16	22	AAV98965	Immunostimulatory
41	13	65.0	17	19	AAV19659	Human bcl-2 antis
42	13	65.0	18	16	AAQ86659	Bcl-2 antisense ol
43	13	65.0	18	19	AAV52545	Unmethylated CpG d
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ALIGNMENTS

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DT	27-SEP-1995 (first entry)	
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DE	Bcl-2 translation initiation site region.	
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KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;	
KW	Lymphoma; programmed cell death; ss.	
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OS	Synthetic.	
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PN	W09508350-A.	
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PD	30-MAR-1995.	
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PF	20-SEP-1994; 94MO-US10725.	
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PR	20-SEP-1993; 93US-0124256.	
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DR	WPI; 1995-139394/18.	
XX		
PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment	
PT	of human solid tumours, esp. breast cancer	
XX		

PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA08650-55) or the 5'-cap
CC region (AA08656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
CC (AA086649) was used as a control.
XX
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcctctccc 20
|||||
DB 20 CAGCGTGCCTCTCTCCC 1

RESULT 2

AAV19651
ID AAV19651 standard; DNA; 20 BP.

AC AAV19651;

DE 12-JUN-1998 (first entry)

DE Human bcl-2 antisense oligonucleotide 1.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
cancer; ss.

OS Synthetic.
OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 6; Columns 3-4; 21pp; English.

XX This antisense oligonucleotide is complementary to the translation
CC initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC oligonucleotides are phosphorothioate derivatives and can straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of
CC a functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcctctccc 20
|||||
DB 1 cagcgtgcgcctctccc 20

RESULT 3

AAV19657/C
ID AAV19657 standard; DNA; 20 BP.

AC AAV19657;

DE 12-JUN-1998 (first entry)

DE Human bcl-2 transcription initiation sense (TI-S) oligonucleotide.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
cancer; ss.

OS Synthetic.
OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Disclosure; Column 19; 21pp; English.

XX This oligonucleotide is used as a control in measuring DNA fragmentation
CC as an indicator of bcl-2 antisense oligonucleotide mediated programmed
CC cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
CC straddle strategic sites such as the translation initiation site, donor
CC and acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcctctccc 20
|||||
DB 20 CAGCGTGCCTCTCTCCC 1

RESULT 4

AAV15276
ID AAV15276 standard; DNA; 20 BP.

AC AAV15276;

DE 15-NOV-2001 (first entry)

```
XX DE Human Bcl-2 mRNA targeted liposomal antisense oligonucleotide #1.
XX KW Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; antisense;
XX KW chronic lymphocytic leukaemia; plasma cell dyscrasia; cancer; pancreas;
XX KW breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
XX KW testes; skin; head; kidney; colon; immune disorder; liposome; ss.
XX OS Homo sapiens.
XX PN WO200160998-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US40159.
XX PR 18-FEB-2000; 2000US-0506979.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Tait AM, Lopez-Berestein G, Gutierrez-Puente Y;
XX DR WPI; 2001-529911/58.
XX PT Compositions comprising short antisense oligonucleotides and a lipid
XX PT component, useful for treating Bcl-associated diseases, e.g. cancer -
XX PS Example 1; Page 31; 63pp; English.
XX CC The invention relates to a liposomal composition of antisense
XX CC oligonucleotides targeted to the translation initiation site of human
XX CC Bcl-2 mRNA. The invention also relates to a method useful for treating
XX CC Bcl-associated diseases like cancer such as follicular and nonfollicular
XX CC lymphomas, chronic lymphocytic leukaemia and plasma cell dyscrasias;
XX CC solid tumours like those associated with breast, prostate, liver,
XX CC pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
XX CC stomach, kidney and colon cancer; and immune disorders. The present DNA
XX CC sequence is liposomal antisense oligonucleotide targeted to the
XX CC translation initiation site of human Bcl-2 mRNA. This antisense
XX CC oligonucleotide which is preferably composed of a nuclease resistant
XX CC backbone is able to inhibit the production of Bcl-2 protein.
XX SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
Db 1 cagcgtgcgcacatcctccc 20

RESULT 5
AADI2300/C
ID AADI2300 standard; DNA; 20 BP.
XX AC AADI2300;
XX DT 06-NOV-2001 (first entry)
XX DE AM-TIS sulphate-oligonucleotide to detect binding of charged species.
XX KW AM-TIS sulphate-oligonucleotide; DNA transfection; fluorophore;
XX KW biomolecule; charged species; lipid vesicle; ss.
XX OS unidentified.
XX FH key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /mod_base= OTHER
```

```
FT FT /note="Optionally labelled with FITC
FT FT (fluoresceinisochoyanate)"
FT FT modified_base 1.20
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "Sulphate-Oligodeoxynucleotide"
XX PN WO200159156-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-IL00134.
XX PR 10-FEB-2000; 2000US-0181693.
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Barenholz Y, Hirsch-Jerner D, Cohen R, Dagan A, Gatt S;
XX DR WPI; 2001-497084/54.
XX PT Determining binding of compounds to a surface, particularly of DNA to
XX PT transfection vesicle, using lipid-coupled fluorophore as pH- or
XX PT potential-sensitive probe -
XX PS Example 4; Page 20; 39pp; English.
XX CC The invention relates to a method for determining the binding of a
XX CC species at a surface, where binding alters the local pH or the surface
XX CC potential, by stable incorporation of a probe at the surface. Probe
XX CC consists of a pH- or potential-sensitive fluorophore attached to either
XX CC a steroid or a lipid having at least two alkyl or alkenyl chains of at
XX CC least 14 carbons. A change in fluorescence from fluorophore when a
XX CC species binds to, or is released from, the surface is detected.
XX CC The method is used for determining the extent of binding of species,
XX CC particularly a biomolecule (nucleic acid or protein) to a surface or its
XX CC release from the surface. Particularly the surface is a lipid vesicle
XX CC being used for DNA transfection or a cell membrane. The method is also
XX CC useful for monitoring transfection of DNA to cells, in vivo or in vitro.
XX CC The method is used for detecting both specific and non-specific
XX CC interactions at the surface. The lipid/steroid component ensures stable
XX CC incorporation of the probe, thus stable and reproducible observation of
XX CC interactions. The present DNA sequence is an AM-TIS sulphate-
XX CC oligodeoxynucleotide which is used to detect the binding of charged
XX CC species.
XX SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
Db 20 CAGCCTGCGCCATCCTTCCC 1

RESULT 6
AADI2301
ID AADI2301 standard; DNA; 20 BP.
XX AC AADI2301;
XX DT 06-NOV-2001 (first entry)
XX DE Bcl2-TIAS sulphate-oligonucleotide to detect binding of charged species.
XX KW Bcl2-TIAS sulphate-oligonucleotide; DNA transfection; fluorophore;
XX KW biomolecule; charged species; lipid vesicle; ss.
XX OS unidentified.
```

```

FH Key Location/Qualifiers
FT modified_base 1
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Optionally labelled with FITC
FT FT (fluoresceinisochoyanate)"
FT modified_base 1..20
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "Sulphate-Oligodeoxynucleotide"
XX
XX WO200159156-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-1100134.
XX
XX 10-FEB-2000; 2000US-0181693.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Barenholz Y, Hirsch-Ierner D, Cohen R, Dagan A, Gatt S;
XX WPI; 2001-497084/54.
XX
XX Determining binding of compounds to a surface, particularly of DNA to
XX transfection vesicle, using lipid-coupled fluorophore as pH- or
XX potential-sensitive probe
XX
XX Example 4; Page 20; 39pp; English.
XX
XX The invention relates to a method for determining the binding of a
XX species at a surface, where binding alters the local pH or the surface
XX potential, by stable incorporation of a probe at the surface. Probe
XX consists of a pH- or potential-sensitive fluorophore attached to either
XX a steroid or a lipid having at least two alkyl or alkenyl chains of at
XX least 14 carbons. A change in fluorescence from fluorophore when a
XX species binds to, or is released from, the surface is detected.
XX The method is used for determining the extent of binding of species,
XX particularly a biomolecule (nucleic acid or protein) to a surface or its
XX release from the surface. Particularly the surface is a lipid vesicle
XX being used for DNA transfection or a cell membrane. The method is also
XX useful for monitoring transfection of DNA to cells, in vivo or in vitro.
XX The method is used for detecting both specific and non-specific
XX interactions at the surface. The lipid/steroid component ensures stable
XX incorporation of the probe, thus stable and reproducible observation of
XX interactions. The present DNA sequence is an Bcl2-TTAS sulphate-
XX Oligodeoxynucleotide which is used to detect the binding of charged
XX species.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
SQ
XX
XX Query Match 100.0%; Score 20; DB 22; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.5;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 cagcgtgcgcacccctccc 20
XX 1 cagcgtgcgcacccctccc 20
XX
XX RESULT 7
XX AAF77808
XX ID AAF77808 standard; DNA; 20 BP.
XX
XX AAF77808;
XX
XX 29-MAY-2001 (first entry)
XX
XX BCL-2 antisense oligodeoxynucleotide.
XX
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
XX

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```

XX
XX Unidentified.
XX
XX OS
XX PN WO200113914-A1.
XX
XX PD 01-MAR-2001.
XX
XX 22-AUG-2000; 2000WO-US22957.
XX
XX PR 24-AUG-1999; 99US-0379718.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
XX Farrell NP;
XX
XX WPI; 2001-257588/26.
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
XX cancers, involves forming a complex comprising the oligodeoxynucleotide
XX and a polynuclear platinum compound, and providing the complex to the
XX cells
XX
XX Example 1; Page 27; 52pp; English.
XX
XX The present invention relates to a method for delivering an antisense
XX oligodeoxynucleotide to cells. The method comprises forming a complex
XX comprising the antisense oligonucleotide and a polynuclear platinum
XX compound, and providing the complex to the cells. The present sequence is
XX an antisense oligonucleotide for BCL-2, which may be used in the present
XX invention. BCL-2 is a suppressor of apoptosis and its expression in
XX cancer cells may contribute to the resistance of cancer cells to
XX apoptosis. The complex of the present invention is useful for treating
XX cancer and any other disease amenable to the treatment by antisense
XX oligonucleotides.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
SQ
XX
XX Query Match 100.0%; Score 20; DB 22; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.5;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 cagcgtgcgcacccctccc 20
XX 1 cagcgtgcgcacccctccc 20
XX
XX RESULT 8
XX AAF77809/C
XX ID AAF77809 standard; DNA; 20 BP.
XX
XX AAF77809;
XX
XX 29-MAY-2001 (first entry)
XX
XX Control sense oligodeoxynucleotide.
XX
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
XX
XX Unidentified.
XX
XX WO200113914-A1.
XX
XX 01-MAR-2001.
XX
XX 22-AUG-2000; 2000WO-US22957.
XX
XX PR 24-AUG-1999; 99US-0379718.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
XX Farrell NP;
XX

```


DR WPI: 2001-257588/26.
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
PT cancers, involves forming a complex comprising the oligodeoxynucleotide
PT and a polynuclear platinum compound, and providing the complex to the
PT cells
XX
XX Example 4; Page 28; 52pp; English.
XX
XX The present invention relates to a method for delivering an antisense
CC oligodeoxynucleotide to cells. The method comprises forming a complex
CC comprising the antisense oligonucleotide and a polynuclear platinum
CC compound, and providing the complex to the cells. The present sequence is
CC a control sense oligonucleotide which was used in an assay for BCL-2
CC antisense oligonucleotide activity (see AAF77808). BCL-2 is a suppressor
CC of apoptosis and its expression in cancer cells may contribute to the
CC resistance of cancer cells to apoptosis. The complex of the present
CC invention is useful for treating cancer and any other disease amenable to
CC the treatment by antisense oligonucleotides.
XX
XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttccc 20
|||||
DB 20 CAGCGTGCACCATCTTCCC 1

RESULT 9
AAQ49816
ID AAQ49816 standard; DNA; 22 BP.
XX
XX AAQ49816;
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX W09320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PF
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX
XX 02-APR-1992; 92GB-0007276.
PR
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing BCL-2
XX
XX
XX Disclosure; Page 58; 109pp; English.
PS
XX
XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.

CC of bcl-2 antisense oligonucleotides.
XX
XX Sequence 22 BP; 2 A; 12 C; 4 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttccc 20
|||||
DB 3 cagcgtgcgcacatcttccc 22

RESULT 10
AAQ49817
ID AAQ49817 standard; RNA; 22 BP.
XX
XX AAQ49817;
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX W09320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PF
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX
XX 02-APR-1992; 92GB-0007276.
PR
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing BCL-2
XX
XX
XX Disclosure; Page 58; 109pp; English.
PS
XX
XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.
XX
XX Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;
SQ

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttccc 20
|||||
DB 3 cagcgtgcgcacacuuucc 22

RESULT 11
AAQ86644/C
ID AAQ86644 standard; DNA; 35 BP.
XX

AC AA086644;
XX
DT 27-SEP-1995 (first entry)
XX
DE Bcl-2 translation initiation region.
XX
KW Antisense oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KW ss.
XX
OS Synthetic.
XX
PN WO9508350-A.
XX
PD 30-MAR-1995.
XX
PF 20-SEP-1994; 94WO-US10725.
XX
PR 20-SEP-1993; 93US-0124256.
XX
PA (REED/) REED J C.
XX
PI Reed JC;
XX
DR WPI; 1995-139394/18.
XX
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Disclosure; Page 13; 108pp; English.
XX
CC The antisense oligonucleotide TI-AS (AA086643) straddles the
CC translation-initiation site in the mRNA coding strand of the human
CC bcl-2 gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells. The corresp. sense bcl-1 sequence
CC was synthesized for use as a control.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcgtgcgcacatcctccc 20
DB 30 CAGCGTGCACATCCTTCCC 11
RESULT 12
AAV19652/C
ID AAV19652 standard; DNA; 35 BP.
XX
XX AAV19652;
XX
XX 12-JUN-1998 (first entry)
XX
DE Human bcl-2 oligonucleotide 1.
XX
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX US5734033-A.
XX
XX 31-MAR-1998.
XX
XX 24-MAR-1994; 94US-0288692.
XX
XX 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.
PR 24-MAR-1994; 94US-0217082.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
PI Reed J;
XX
DR WPI; 1998-229881/20.
XX
PT Anti-sense oligo(nucleotide(s) complementary to BCL-2 mRNA - useful
PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
XX Claim 1; Columns 3-4; 21pp; English.
XX
CC This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the translation initiation site of the
CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
CC straddle strategic sites such as the translation initiation site, donor
CC and acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcgtgcgcacatcctccc 20
DB 30 CAGCGTGCACATCCTTCCC 11
RESULT 13
AAC86407
ID AAC86407 standard; RNA; 20 BP.
XX
XX AAC86407;
XX
XX 28-FEB-2001 (first entry)
XX
DE Human bcl-XL and bcl-2 mRNA antisense control sequence C02.
XX
XX Human; bcl-XL; bcl-2; apoptosis; antisense; cancer; allergic disease;
KW restenosis; fibrosis; psoriasis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200066724-A2.
XX
XX 09-NOV-2000.
XX
XX 26-APR-2000; 2000WO-EP03708.
XX
XX 30-APR-1999; 99GB-0010119.
XX
XX (UYZU-) UNIV ZUERICH.
XX
XX Zangemeister-Wittke U, Luedke G, Huesken D;
PI
XX
DR WPI; 2001-015981/02.
XX
XX Antisense oligonucleotide derivatives directed against human bcl-XL
XX mRNA and capable of modulating biosynthesis of human bcl-XL proteins,
XX useful in treatment and diagnosis of hyperproliferative diseases -
XX
XX Example 2; Page 23; 38pp; English.
XX
XX The present invention provides antisense nucleotides which hybridise to
CC the human bcl-XL and bcl-2 mRNA sequences. The bcl-XL and bcl-2 proteins

are involved in apoptosis, and the antisense strands can be used to inhibit them and possibly lead to cell death. The nucleic acids of the invention can be used in the treatment of cancer, particularly colorectal, gastric, prostate, thyroid, renal, breast and lung cancers, neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain types of allergic disease.

Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 95.0%; Score 19; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccaccccttc 19
|||||
Db 2 cagcgtgcccaccccttc 20

RESULT 14

ID AAV11591 standard; DNA; 18 BP.

AC AAV11591;

DT 30-JUL-1998 (first entry)

DE Liposomal bcl-2 antisense polynucleotide.

KW Bcl-2; antisense; disease; treatment; cancer; follicular lymphoma; leukemia; plasma cell dyscrasia; breast; prostate; colon; autoimmune diseases; ss.

OS Synthetic.

XX Homo sapiens.

PN W09814172-A1.

PD 09-APR-1998.

PF 03-OCT-1997; 97WO-US18348.

PR 04-OCT-1996; 96US-0726211.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Lopez-Berestein G, McDonnell TJ, Tara AM, Tormo M;

DR WPI; 1998-239841/21.

PT Composition comprising oligo:nucleotide anti-sense to Bcl-2 gene - useful for, e.g. treatment of Bcl-2 related disease such as follicular lymphoma and auto-immune disease

PS Claim 4; Page 30; 69pp; English.

CC This sequence is a nuclease-resistant p-ethoxy antisense oligonucleotide which specifically binds to the translation initiation site of human bcl-2 mRNA. This oligonucleotide can be used in a method to treat Bcl-2 related disease in humans and animals, e.g. cancer especially follicular lymphoma (FL), leukemia, plasma cell dyscrasia, cancer of breast, prostate and colon, or autoimmune diseases.

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 90.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccaccccttc 18
|||||
Db 1 cagcgtgcccaccccttc 18

RESULT 15

ID AAC65064 standard; DNA; 21 BP.

AC AAC65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

KW Antisense oligonucleotide; RNA molecule cleavage; immune activation; bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

PN W0200061810-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

PA (OASI-) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal bases, and modified backbone linkages is useful to target therapeutic genes, preferably anti-apoptosis or chemoresistance genes

PS Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides containing a number of degenerate bases and with a modified backbone which can be used to direct cleavage of target RNA molecules. The use of degenerate bases reduces the risk of immune activation following injection into animals, which causes deleterious side effects associated with many therapeutic antisense oligonucleotides. Sequences AAC65029-C65077 are antisense oligonucleotides and PCR primers used in assays to demonstrate the effects of the sequences of the invention.

SO Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match 88.0%; Score 17.6; DB 21; Length 21;
Best Local Similarity 89.5%; Pred. No. 22;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 cagcgtgcccaccccttc 19
|||||
Db 3 cagcgtgcccaccccttc 21

Search completed: June 28, 2002, 22:40:01
Job time: 8077 sec

Mon Jul 1 08:40:43 2002

us-09-709-170a-1.szl75.rng

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 19:58:54 ; Search time 334.55 Seconds
(without alignments)
14,684 Million cell updates/sec

Title: US-09-709-170A-1

Perfect score: 20

Sequence: 1 cagcgtgcgcacatcctccc 20

Scoring table: IDENTITY_NUC

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2-6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2-6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2-6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2-6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2-6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2-6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-217-082A-1
2	20	100.0	20	1	US-08-217-082A-7
3	20	100.0	20	2	US-08-465-485A-1
4	20	100.0	20	2	US-08-465-485A-7
5	20	100.0	20	3	US-09-080-285-1
6	20	100.0	20	3	US-09-080-285-7
7	20	100.0	20	4	US-09-379-718-1
8	20	100.0	20	4	US-09-379-718-2
9	20	100.0	35	1	US-08-217-082A-2
10	20	100.0	35	1	US-08-465-485A-2
11	20	100.0	35	3	US-09-080-285-2
12	17	85.0	17	1	US-08-217-082A-11
13	16	80.0	17	1	US-08-217-082A-10
14	15	75.0	17	1	US-08-217-082A-12
15	13.6	68.0	27	1	US-08-410-804-13
16	13.6	68.0	27	1	US-08-607-269-8
17	13.6	68.0	27	1	US-08-259-514-13
18	13.6	68.0	27	2	US-08-858-311-13
19	13.6	68.0	27	5	PCT-US95-04600-8
20	13.2	66.0	47	4	US-08-869-380-5
21	13.2	66.0	47	4	US-08-869-380-7
22	13.2	66.0	47	5	PCT-US95-13552-16
23	13.2	66.0	47	5	PCT-US95-13552-18
24	13.2	66.0	17	1	US-08-217-082A-9
25	13	65.0	18	1	US-08-217-082A-17
26	13	65.0	18	2	US-08-465-485A-17
27	13	65.0	18	2	US-08-465-485A-24

28	13	65.0	18	3	US-09-080-285-17	Sequence 17, Appl
29	13	65.0	18	3	US-09-080-285-24	Sequence 24, Appl
30	13	65.0	18	3	US-09-249-730-218	Sequence 218, Appl
31	13	65.0	18	3	US-09-118-220-1	Sequence 1, Appl
32	13	65.0	18	3	US-08-738-652-55	Sequence 55, Appl
33	13	65.0	18	4	US-09-030-701-27	Sequence 27, Appl
34	13	65.0	18	4	US-09-286-098-59	Sequence 59, Appl
35	13	65.0	18	4	US-09-286-098-104	Sequence 104, Appl
36	13	65.0	18	4	US-08-960-774-45	Sequence 45, Appl
37	13	65.0	18	4	US-09-078-954-14	Sequence 14, Appl
38	13	65.0	19	6	5276019-8	Patent No. 5276019
39	13	65.0	20	4	US-09-082-649B-60	Sequence 60, Appl
40	12.8	64.0	20	3	US-09-418-640-84	Sequence 84, Appl
41	12.6	63.0	32	4	US-09-272-496-5	Sequence 5, Appl
42	12.4	62.0	45	4	US-08-358-627F-1	Sequence 1, Appl
43	12.2	61.0	21	4	US-09-485-636-25	Sequence 25, Appl
44	12.2	61.0	30	5	PCT-US94-10257A-37	Sequence 37, Appl
45	12.2	61.0	33	3	US-08-816-346-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-217-082A-1
Sequence 1, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatctctccc 20
|||||
Db 1 CAGCGTGCACCATCTCTCCC 20

RESULT 2

US-08-217-082A-7/C
; Sequence 7, Application US/08217082A
; Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITTING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 224 Airport Parkway

CITY: San Jose

STATE: California

COUNTRY: U.S.A.

ZIP: 95110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,082A

FILING DATE: 24-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: Synthetic DNA

ANTI-SENSE: NO

US-08-217-082A-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatctctccc 20
|||||
Db 20 CAGCGTGCACCATCTCTCCC 1

RESULT 3

US-08-465-485A-1
; Sequence 1, Application US/08465485A

Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONF

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES

US-08-465-485A-1

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatctctccc 20
|||||
Db 1 CAGCGTGCACCATCTCTCCC 20

RESULT 4

US-08-465-485A-7/C
; Sequence 7, Application US/08465485A
; Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcgtgcgcacatcctccc 20
DB 20 CAGCGTGCACATCCTCC 1
RESULT 5
US-09-080-285-1
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
DB 1 CAGCGTGCACATCCTCC 20

RESULT 6
US-09-080-285-7/c
Sequence 7, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-7

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatccctcc 20
|||||
DB 20 CAGCGTGCACCATCTCTCC 1

RESULT 7
US-09-379-718-1
Sequence 1, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
TITLE OF INVENTION: Antisense Technology
FILE REFERENCE: Farrell/Kloster
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-1

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatccctcc 20
|||||
DB 1 cagcgtgcgcacatccctcc 20

RESULT 8
US-09-379-718-2/c
Sequence 2, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
TITLE OF INVENTION: Antisense Technology
FILE REFERENCE: Farrell/Kloster
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatccctcc 20
|||||
DB 20 CAGCGTGCACCATCTCTCC 1

RESULT 9
US-08-217-082A-2/c
Sequence 2, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 20; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
Db 30 CAGCGTGGCCATCTCTCC 11

RESULT 10

US-08-465-485A-2/c
Sequence 2, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-2

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
Db 30 CAGCGTGGCCATCTCTCC 11

RESULT 11
US-09-080-285-2/c
Sequence 2, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-2

Query Match 100.0%; Score 20; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
Db 30 CAGCGTGGCCATCTCTCC 11

RESULT 12
US-08-217-082A-11
Sequence 11, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose

STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-11

Query Match 85.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gcgtgcgcacatcttc 19
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DB 1 GCGTGCACATCTTC 17

RESULT 13
US-08-217-082A-10
Sequence 10, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOK, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-10

Query Match 80.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatct 16
|||||
DB 2 CAGCGTGCACATCT 17

RESULT 14
US-08-217-082A-12
Sequence 12, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOK, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:

Search completed: June 28, 2002, 22:16:38
Job time: 8264 sec

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-12

Query Match 75.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 tgcgcacatcttccc 20
Db 1 TGC GCATCTTCCC 15

RESULT 15
US-08-410-804-13/C
Sequence 13, Application US/08410804
Patent No. 5632994
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-410-804-13

Query Match 68.0%; Score 13.6; DB 1; Length 27;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cagcgtgcacatcttccc 20
Db 20 CAGCGTGCACATCTTCCC 1

Mon Jul 1 08:40:44 2002

us-09-709-170a-1.szlm75.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:44 ; Search time 3762.88 seconds

(without alignments)
194.646 Million cell updates/sec

Title: US-09-709-170A-2

Perfect score: 35
Sequence: 1 ctttcctctgggaagatgctgcacacgtggaga 35

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
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32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	35	100.0	35	6	AR052604	AR052604 Sequence
2	35	100.0	35	6	196083	196083 Sequence 2
3	22	62.9	22	6	A76123	A76123 Sequence 3
4	22	62.9	22	6	A76124	A76124 Sequence 4
5	20	57.1	20	6	AR052603	AR052603 Sequence
6	20	57.1	20	6	AR052609	AR052609 Sequence
7	20	57.1	20	6	AR176022	AR176022 Sequence
8	20	57.1	20	6	AR176023	AR176023 Sequence
9	20	57.1	20	6	AX045387	AX045387 Sequence
10	20	57.1	20	6	AX211669	AX211669 Sequence
11	20	57.1	20	6	AX211670	AX211670 Sequence
12	20	57.1	20	6	AX277461	AX277461 Sequence
13	20	57.1	20	6	196082	196082 Sequence 1
14	20	57.1	20	6	196088	196088 Sequence 7
15	19	54.3	19	6	AX083694	AX083694 Sequence
16	18	53.1	18	6	AR004426	AR004426 Sequence
17	18	53.1	18	6	143661	143661 Sequence 13
18	18	53.1	18	6	186720	186720 Sequence 8
19	18	52.6	18	6	AX113708	AX113708 Sequence
20	18	52.6	18	6	AX113709	AX113709 Sequence
21	18	51.4	18	6	AR052619	AR052619 Sequence
22	18	51.4	18	6	AR052624	AR052624 Sequence
23	18	51.4	18	6	AR116926	AR116926 Sequence
24	18	51.4	18	6	AR140496	AR140496 Sequence
25	18	51.4	18	6	AR146347	AR146347 Sequence
26	18	51.4	18	6	AR146392	AR146392 Sequence
27	18	51.4	18	6	AR154716	AR154716 Sequence
28	18	51.4	18	6	AR167448	AR167448 Sequence
29	18	51.4	18	6	AX015198	AX015198 Sequence
30	18	51.4	18	6	AX020948	AX020948 Sequence
31	18	51.4	18	6	AX020954	AX020954 Sequence
32	18	51.4	18	6	AX040169	AX040169 Sequence
33	18	51.4	18	6	AX040403	AX040403 Sequence
34	18	51.4	18	6	AX063576	AX063576 Sequence
35	18	51.4	18	6	AX081353	AX081353 Sequence
36	18	51.4	18	6	AX083693	AX083693 Sequence
37	18	51.4	18	6	AX088930	AX088930 Sequence
38	18	51.4	18	6	AX103809	AX103809 Sequence
39	18	51.4	18	6	AX103862	AX103862 Sequence
40	18	51.4	18	6	AX103863	AX103863 Sequence
41	18	51.4	18	6	AX103899	AX103899 Sequence
42	18	51.4	18	6	AX105211	AX105211 Sequence
43	18	51.4	18	6	AX135635	AX135635 Sequence
44	18	51.4	18	6	AX283183	AX283183 Sequence
45	18	51.4	18	6	AX283250	AX283250 Sequence

ALIGNMENTS

RESULT 1	AR052604	AR052604	35 bp	DNA	linear	PAT 29-SRP-1999
LOCUS	AR052604	Sequence 2 from patent US 5831066.				
DEFINITION	AR052604					
ACCESSION	AR052604					
VERSION	AR052604.1	GI:5975968				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 35)					
AUTHORS	Reed, J.C.					
TITLE	Regulation of bcl-2 gene expression					
JOURNAL	Patent: US 5831066-A 2 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1..35					
BASE COUNT	6 a	8 c	13 g	8 t		
ORIGIN						

Query Match 100.0%; Score 35; DB 6; Length 35;
Best local Similarity 100.0%; Pred. No. 0.00024;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cttctcctggaagatgagcagctggaga 35
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Db 1 CTTTCTCTGGAGAGATGGCGACCTGGAGA 35

RESULT 2
196083
LOCUS Sequence 2 from patent US 5734033. 35 bp DNA linear PAT 01-DEC-1998
ACCESSION 196083
VERSION 196083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..35

BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cttctcctggaagatgagcagctggaga 35
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Db 1 CTTTCTCTGGAGAGATGGCGACCTGGAGA 35

RESULT 3
A76123/c
LOCUS Sequence 3 from Patent WO9320200. 22 bp DNA linear PAT 19-OCT-1999
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan,G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 3 14-OCT-1993;
FEATURES IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

Query Match 62.9%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ggaagatgagcagctgg 32
|||||
Db 22 GGAAGAGATGGCGACGCTGG 1

RESULT 4
A76124/c
LOCUS Sequence 4 from Patent WO9320200. 22 bp DNA linear PAT 19-OCT-1999
DEFINITION

ACCESSION A76124
VERSION A76124.1 GI:6088260
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Evan,G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
FEATURES IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
source Location/Qualifiers
1..22
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/db_xref="taxon:32644"

BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

Query Match 62.9%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ggaagatgagcagctgg 32
|||||
Db 22 GGAAGAGATGGCGACGCTGG 1

RESULT 5
AR052603/c
LOCUS Sequence 1 from patent US 5831066. 20 bp DNA linear PAT 29-SEP-1999
ACCESSION AR052603
VERSION AR052603.1 GI:5975967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 1 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ggaagatgagcagctg 30
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Db 20 GGAAGAGATGGCGACGCTG 1

RESULT 6
AR052609
LOCUS Sequence 7 from patent US 5831066. 20 bp DNA linear PAT 29-SEP-1999
DEFINITION AR052609
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES Location/Qualifiers

source 1.20
/organism="unknown"
BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcagctg 30
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1 GGGAAGATGCGCACGCTG 20

RESULT 7
LOCUS AR176022 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcagctg 30
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20 GGGAAGATGCGCACGCTG 1

RESULT 8
LOCUS AR176023 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023
VERSION AR176023.1 GI:17917322
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcagctg 30

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Db 1 GGGAAGATGCGCACGCTG 20

RESULT 9
LOCUS AX045387/c 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 7 from Patent WO0066724.
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zangemeister-Wilke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mRNA
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 gggaagatgagcagcagctg 31
|||||
20 GGGAAGATGCGCACGCTGG 1

RESULT 10
LOCUS AX211669 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 1 from Patent WO0159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatl,S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note=""

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcagctg 30
|||||
1 GGGAAGATGCGCACGCTG 20

RESULT 11
AX211670/c
LOCUS AX211670 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 2 from Patent WO0159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 20)
Barenholz, Y., Hirsch-Ierner, D., Cohen, R., Dagan, A. and Gatt, S.
Detection of binding of charged species using ph- or
potential-sensitive probes
Patent: WO 0159156-A 2 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem
(IL)
FEATURES
SOURCE
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note=".".
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGGAGGATGGCGACGCTG 1

RESULT 12
AX277461/c
LOCUS AX277461 20 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0160998.
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
synthetic construct
artificial sequence.
1 (sites)
Tari, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
Small oligonucleotides with anti-tumor activity
Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)
FEATURES
SOURCE
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Primer."
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGGAGGATGGCGACGCTG 1

RESULT 13
196082/c
LOCUS 196082 20 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5734033.
ACCESSION 196082

VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Reed, J.
Antisense oligonucleotides inhibiting human bcl-2 gene expression
Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGGAGGATGGCGACGCTG 1

RESULT 14
196088
LOCUS 196088 20 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5734033.
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Reed, J.
Antisense oligonucleotides inhibiting human bcl-2 gene expression
Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 gggaagatggcgacgctg 30
|||||
Db 1 GGGAGGATGGCGACGCTG 20

RESULT 15
AX083694/c
LOCUS AX083694 19 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0110468.
ACCESSION AX083694
VERSION AX083694.1 GI:13185422
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 19)
Papisov, M.I.
Drug-carrier complexes and methods of use thereof
Patent: WO 0110468-A 8 15-FEB-2001;
THE GENERAL HOSPITAL CORPORATION (US)
Location/Qualifiers
1..19
/organism="synthetic construct"
BASE COUNT 19 a 10 c 4 g 4 t
ORIGIN

/db_xref="taxon:32630"
 /note="Synthetic Oligonucleotide-c indicates an RNA base"
 BASE COUNT 2 a 9 c 4 g 4 t
 ORIGIN

Query Match 54.3%; Score 19; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 gatggcgacgcctggaga 35
 ||||||||||||||||
 Db 19 GATGGCGCACGCTGGGAGA 1

Search completed: June 28, 2002, 22:10:45
 Job time: 8336 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:01 ; Search time 1381.16 Seconds
(Without alignments)
43.508 Million cell updates/sec

Title:	US-09-709-170A-2
Perfect score:	35

Sequence: 1 ctttctctggaagatgctgcacgctggaga 35

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

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Minimum DB seq length: 0
Maximum DB seq length: 75
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	35	100.0	35	16	AAO86644	Bcl-2 translation
2	35	100.0	35	19	AAV19652	Human bcl-2 oligon
3	22	62.9	22	14	AAO49816	Bcl-2 antisense o
4	22	62.9	22	14	AAO49817	Bcl-2 antisense o
5	20	57.1	20	16	AAO86649	Bcl-2 translation
6	20	57.1	20	19	AAV19651	Human bcl-2 antis
7	20	57.1	20	19	AAV19657	Human bcl-2 trans
8	20	57.1	20	22	AAI15766	Human bcl-2 mRNA t
9	20	57.1	20	22	AAI13300	Human Bcl-2 transla

C	10	20	57.1	20	22	AAJ12301	B2-TTAS sulphate
C	11	20	57.1	20	22	AAJ77808	BCL-2 antisense ol
C	12	20	57.1	20	22	AAJ77809	Control sense olig
C	13	20	57.1	20	22	AAJ66407	Human bcl-xl and b
C	14	19.6	56.0	21	21	AAJ65064	Human bcl genes an
C	15	19	54.3	19	20	AAJ06730	Antisense oligomer
C	16	19	54.3	36	22	AAJ45307	Human Bcl-2 PCR pr
C	17	18.6	53.1	27	17	AAJ18388	Human Bcl-2 forwan
C	18	18.4	52.6	60	22	AAJ64517	PCR primer used to
C	19	18.4	52.6	70	22	AAJ68518	PCR primer used to
C	20	18	51.4	18	16	AAJ086659	Bcl-2 antisense ol
C	21	18	51.4	18	19	AAJ52545	Unmethylated Cpg d
C	22	18	51.4	18	19	AAJ27719	Immunostimulatory
C	23	18	51.4	18	19	AAJ28181	Antisense oligonuc
C	24	18	51.4	18	19	AAJ11567	Liposomal bcl-2 an
C	25	18	51.4	18	19	AAJ19667	Human bcl-2 antis
C	26	18	51.4	18	20	AAJ31944	Cpg adjuvant oligo
C	27	18	51.4	18	20	AAJ241905	IL-12 secretion in
C	28	18	51.4	18	20	AAJ241948	IL-12 secretion in
C	29	18	51.4	18	20	AAJ78803	HPV fusion protein
C	30	18	51.4	18	20	AAJ85837	Cytosine-quanosine
C	31	18	51.4	18	20	AAJ33514	BCL2-targeted anti
C	32	18	51.4	18	20	AAJ23693	Deletion sequence
C	33	18	51.4	18	20	AAJ27536	Synthetic RNA sequ
C	34	18	51.4	18	20	AAJ18702	Target bcl-2 antise
C	35	18	51.4	18	20	AAJ99434	Antisense oligonuc
C	36	18	51.4	18	21	AAJ64137	Immunostimulatory
C	37	18	51.4	18	21	AAJ60278	Immunostimulatory
C	38	18	51.4	18	21	AAJ65037	Bcl2 antisense sec
C	39	18	51.4	18	21	AAJ90450	Cpg adjuvant oligo
C	40	18	51.4	18	21	AAJ91620	Human Bcl-2 antise
C	41	18	51.4	18	21	AAJ39264	Cpg immunostimula
C	42	18	51.4	18	21	AAJ14470	Phosphorothioate c
C	43	18	51.4	18	21	AAJ38517	Oligonucleotide us
C	44	18	51.4	18	21	AAJ29003	Cpg motif for immu
C	45	18	51.4	18	21	AAJ60975	Nucleotide sequen

ALIGNMENTS

XX	RESULT	1
XX	ID	AA086644
XX		AA086644 standard; DNA; 35 BP.
XX	AC	AA086644;
XX	DT	27-SEP-1995 (first entry)
XX	DE	Bcl-2 translation initiation region.
XX	XX	Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy
XX	KW	leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
XX	SS.	
XX	OS	Synthetic.
XX	PN	WO9508350-A.
XX	PD	30-MAR-1995.
XX	PF	20-SEP-1994; 94WO-US10725.
XX	PR	20-SEP-1993; 93US-0124256.
XX	PA	(REED/) REED J C.
XX	PI	Reed JC;
XX	DR	WPI; 1995-139394/18.
XX	PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX		of human solid tumours, esp. breast cancer

XX Disclosure; Page 13; 108pp; English.
PS
XX
CC The antisense oligonucleotide T1-AS (AA086643) straddles the
CC translation-initiation site in the mRNA coding strand of the human
CC bcl-2 gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells. The corresp. sense bcl-1 sequence
CC was synthesized for use as a control.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 35; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cttctctcgggaagatgacgcacgtcgagaga 35
Db 1 cttctctcgggaagatgacgcacgtcgagaga 35

RESULT 2

AAV19652
ID AAV19652 standard; DNA: 35 BP.

AC AAV19652;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 1.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

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Query Match 100.0%; Score 35; DB 19; Length 35;

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cttctctcgggaagatgacgcacgtcgagaga 35
Db 1 cttctctcgggaagatgacgcacgtcgagaga 35

RESULT 3

AAQ49816/C
ID AAQ49816 standard; DNA: 22 BP.

AC AAQ49816;

DT 03-MAY-1994 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;

KW expression; myc; ss.

OS Synthetic.

PN W03320200-A.

PD 14-OCT-1993.

PF 02-APR-1993; 93WO-GB00686.

PR 02-APR-1992; 92GB-0007275.

PR 02-APR-1992; 92GB-0007276.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

PI Evan GT;

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XX

XX

XX

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XX

Query Match 62.9%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 gggaagatgacgcacgtcgag 32
Db 22 GGGAAGATGACGCACGCTGGG 1

RESULT 4

AAQ49817/C
ID AAQ49817 standard; RNA: 22 BP.

AC AAQ49817;

DT 03-MAY-1994 (first entry)

DE Bcl-2 antisense oligonucleotide.

KM Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
 KM expression; myc; ss.
 OS Synthetic.
 PN W09320200-A.
 PD 14-OCT-1993.
 PF 02-APR-1993; 93WO-GB00686.
 PR 02-APR-1992; 92GB-0007275.
 PR 02-APR-1992; 92GB-0007276.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PI Evan GI;
 PT WPI; 1993-336908/42.
 PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
 PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
 PT antisense oligo:nucleotide(s), also increasing survival of
 PT cultured cells by expressing Bcl-2
 PS Disclosure: Page 58; 109pp; English.
 CC A DNA construct comprising the bcl-2 coding sequence under control
 CC of elements allowing its expression is claimed. Myc-induced cell
 CC death can be inhibited in cultured cells by expressing bcl-2.
 CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
 CC of bcl-2 antisense oligonucleotides.
 CC
 SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;
 QY 11 gggaagatgagcagcagctgg 32
 Db 22 GCGAAGATGCGCGCAGCTGGG 1
 RESULT 5
 AA086649
 ID AA086649 standard; DNA; 20 BP.
 AC AA086649;
 XX 27-SEP-1995 (first entry)
 DE Bcl-2 translation initiation site region.
 KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW lymphoma; programmed cell death; ss.
 OS Synthetic.
 PN W09508350-A.
 PD 30-MAR-1995.
 PF 20-SEP-1994; 94WO-US10725.
 PR 20-SEP-1993; 93US-0124256.
 PA (REED/) REED J C.
 PI Reed JC;
 DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 PS Example 12; Page 33; 108pp; English.
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS1846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA08650-55) or the 5'-cap
 CC region (AA08656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
 CC (AA086649) was used as a control.
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
 QY 11 gggaagatgagcagcagctg 30
 Db 1 gggaagatgagcagcagctg 20
 RESULT 6
 AA019651/C
 ID AA019651 standard; DNA; 20 BP.
 AC AA019651;
 XX 12-JUN-1998 (first entry)
 DE Human bcl-2 antisense oligonucleotide 1.
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 KW cancer; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN US5734033-A.
 PD 31-MAR-1998.
 PF 24-MAR-1994; 94US-0288692.
 PR 21-FEB-1992; 92US-0840716.
 PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 PA (UYPE-) UNIV PENNSYLVANIA.
 PI Reed J;
 DR WPI; 1998-229881/20.
 KW Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 KW for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 OS Claim 6; Columns 3-4; 21pp; English.
 CC This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of
 CC a functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 19; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 20 GGGAGAGATGGCGCAGCTG 1

RESULT 7

AAV19657
AAV19657 standard; DNA; 20 BP.

AC AAV19657;

DE 12-JUN-1998 (first entry)

DE Human bcl-2 transcription initiation sense (T1-S) oligonucleotide.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukemia; human;

OS Cancer; ss.

OS Synthetic.

OS Homo sapiens.

FN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
for treating cancers, e.g. lymphoma(s) and some Leukemia(s)
PS Disclosure; Column 19; 21pp; English.

CC This oligonucleotide is used as a control in measuring DNA fragmentation
CC as an indicator of bcl-2 antisense oligonucleotide mediated programmed
CC cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
CC straddle strategic sites such as the translation initiation site, donor
CC and acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukemias.
XX

Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 19; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 1 ggaagagatgagcagcagctg 20

RESULT 8

AAAD15276/c
ID AAAD15276 standard; DNA; 20 BP.

XX
AC AAAD15276;

DE 15-NOV-2001 (first entry)

DE Human Bcl-2 mRNA targeted liposomal antisense oligonucleotide #1.

KW Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; antisense;
KW chronic lymphocytic leukemia; plasma cell dyscrasia; cancer; pancreas;
KW breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
KW testes; skin; head; kidney; colon; immune disorder; liposome; ss.
OS Homo sapiens.

FN WO200160998-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US40159.

PR 18-FEB-2000; 2000US-0506979.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Tari AM, Lopez-Berestein G, Gutierrez-Puente Y;

DR WPI; 2001-529911/58.

PT Compositions comprising short antisense oligonucleotides and a lipid
component, useful for treating Bcl-associated diseases, e.g. cancer -
XX
XX Example 1; Page 31; 63pp; English.

CC The invention relates to a liposomal composition of antisense
CC oligonucleotides targeted to the translation initiation site of human
CC Bcl-2 mRNA. The invention also relates to a method useful for treating
CC Bcl-associated diseases like cancer such as follicular and nonfollicular
CC lymphomas, chronic lymphocytic leukemia and plasma cell dyscrasias;
CC solid tumours like those associated with breast, prostate, liver,
CC pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
CC stomach, kidney and colon cancer; and immune disorders. The present DNA
CC sequence is liposomal antisense oligonucleotide targeted to the
CC translation initiation site of human Bcl-2 mRNA. This antisense
CC oligonucleotide which is preferably composed of a nuclease resistant
CC backbone is able to inhibit the production of Bcl-2 protein.
XX

Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 22; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 20 GGGAGAGATGGCGCAGCTG 1

RESULT 9

AAAD12300
ID AAAD12300 standard; DNA; 20 BP.

AC AAAD12300;

DE 06-NOV-2001 (first entry)

DE AM-TIS sulphate-oligonucleotide to detect binding of charged species.

KW AM-TIS sulphate-oligonucleotide; DNA transfection; fluorophore;

KW biomolecule; charged species; lipid vesicle; ss.

OS Unidentified.

XX BCL-2 antisense oligodeoxynucleotide.
DE
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
KM
XX Unidentified.
OS
XX WO200113914-A1.
PN
XX
XX
XX 01-MAR-2001.
PD
XX
XX 22-AUG-2000; 2000WO-US22957.
PF
XX
XX 24-AUG-1999; 99US-0379718.
PR
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
PA
XX
XX
XX Farrell NP;
PI
XX
XX WPI; 2001-257588/26.
DR
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
PT
XX cancers, involves forming a complex comprising the oligodeoxynucleotide
PT and a polynuclear platinum compound, and providing the complex to the
PT cells
XX
XX
XX Example 1; Page 27; 52pp; English.
PS
XX
XX The present invention relates to a method for delivering an antisense
CC oligodeoxynucleotide to cells. The method comprises forming a complex
CC comprising the antisense oligonucleotide and a polynuclear platinum
CC compound, and providing the complex to the cells. The present sequence is
CC an antisense oligonucleotide for BCL-2, which may be used in the present
CC invention. BCL-2 is a suppressor of apoptosis and its expression in
CC cancer cells may contribute to the resistance of cancer cells to
CC apoptosis. The complex of the present invention is useful for treating
CC cancer and any other disease amenable to the treatment by antisense
CC oligonucleotides.
CC
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;
SQ

Query Match 57.1%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcgacgctg 30
|||||
Db 20 GGGAAGATGCGCACGCTG 1

RESULT 12
AAF77809
ID AAF77809 standard; DNA; 20 BP.
XX
XX AAF77809;
AC
XX
XX 29-MAY-2001 (first entry)
DT
XX
XX Control sense oligodeoxynucleotide.
DE
XX
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
KM
XX
XX Unidentified.
OS
XX
XX WO200113914-A1.
PN
XX
XX 01-MAR-2001.
PD
XX
XX 22-AUG-2000; 2000WO-US22957.
PF
XX
XX 24-AUG-1999; 99US-0379718.
PR
XX
XX

PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
XX Farrell NP;
PI
XX
XX WPI; 2001-257588/26.
DR
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
PT
XX cancers, involves forming a complex comprising the oligodeoxynucleotide
PT and a polynuclear platinum compound, and providing the complex to the
PT cells
XX
XX
XX Example 4; Page 28; 52pp; English.
PS
XX
XX The present invention relates to a method for delivering an antisense
CC oligodeoxynucleotide to cells. The method comprises forming a complex
CC comprising the antisense oligonucleotide and a polynuclear platinum
CC compound, and providing the complex to the cells. The present sequence is
CC a control sense oligonucleotide which was used in an assay for BCL-2
CC antisense oligonucleotide activity (see AAF77808). BCL-2 is a suppressor
CC of apoptosis and its expression in cancer cells may contribute to the
CC resistance of cancer cells to apoptosis. The complex of the present
CC invention is useful for treating cancer and any other disease amenable to
CC the treatment by antisense oligonucleotides.
CC
XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
SQ

Query Match 57.1%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcgacgctg 30
|||||
Db 1 gggaagatgagcgacgctg 20

RESULT 13
AAC86407/C
ID AAC86407 standard; RNA; 20 BP.
XX
XX AAC86407;
AC
XX
XX 28-FEB-2001 (first entry)
DT
XX
XX Human bcl-xl and bcl-2 mRNA antisense control sequence CO2.
DE
XX
XX Human: bcl-xl; bcl-2; apoptosis; antisense; cancer; allergic disease;
KM restenosis; fibrosis; psoriasis; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200066724-A2.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 26-APR-2000; 2000WO-EP03708.
PF
XX
XX 30-APR-1999; 99GB-0010119.
PR
XX
XX (UYZU-) UNIV ZUERICH.
PA
XX
XX Zangemeister-Wittke U, Luedke G, Huesken D;
PI
XX
XX WPI; 2001-015981/02.
DR
XX
XX Antisense oligonucleotide derivatives directed against human bcl-xl
PT mRNA and capable of modulating biosynthesis of human bcl-xl proteins,
PT useful in treatment and diagnosis of hyperproliferative diseases -
XX
XX Example 2; Page 23; 38pp; English.
PS
XX
XX The present invention provides antisense nucleotides which hybridise to
CC the human bcl-xl and bcl-2 mRNA sequences. The bcl-xl and bcl-2 proteins

CC are involved in apoptosis, and the antisense strands can be used to
CC inhibit them and possibly lead to cell death. The nucleic acids of the
CC invention can be used in the treatment of cancer, particularly
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
CC types of allergic disease.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 57.1%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 ggaagatgagcagctgg 31
|||||
DB 20 GGAGGATGGCGACGCTGG 1

RESULT 14

AAC65064/C
ID AAC65064 standard; DNA; 21 BP.

AC AAC65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

KM Antisense oligonucleotide; RNA molecule cleavage; immune activation;
bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

PN WO200061810-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

PA (OASIS) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal
bases, and modified backbone linkages is useful to target therapeutic

PT genes, preferably anti-apoptosis or chemoresistance genes

PS Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
CC containing a number of degenerate bases and with a modified backbone

CC which can be used to direct cleavage of target RNA molecules. The use of
CC degenerate bases reduces the risk of immune activation following

CC injection into animals, which causes deleterious side effects associated
CC with many therapeutic antisense oligonucleotides. Sequences

CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
CC assays to demonstrate the effects of the sequences of the invention.

XX
SQ Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match 56.0%; Score 19; DB 21; Length 21;
Best Local Similarity 90.5%; Pred. No. 64;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 ggaagatgagcagctgg 32
|||||
DB 21 GGAARNATGGCGACGCTGG 1

RESULT 15

AAZ06730/C
ID AAZ06730 standard; DNA; 19 BP.

AC AAZ06730;

DT 23-NOV-1999 (first entry)

DE Antisense oligomer used to determine role of Bcl-2.

KM p75NTR; p75 neurotrophin receptor; nerve growth factor;

KM NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;

KM Alzheimer's disease; pseudo-ligand; hair growth; hair colour;

KM skin colour; alopecia areata; male pattern baldness; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9939728-A2.

PD 12-AUG-1999.

PF 03-FEB-1999; 99WO-US02362.

PR 04-FEB-1998; 98US-0018194.

PA (UYBO-) UNIV BOSTON.

PI Eller M, Gilchrist BA, Yaar M;

DR WPI; 1999-539950/45.

PT Controlling or manipulating melanocyte and keratinocyte cell death,
useful for treating, e.g. alopecia areata

PS Example 8; Page 32; 67pp; English.

CC Sequences AAZ06728-706729 are used to determine the role of the p75

CC nerve growth factor receptor (p75-NGFR/p75NTR) in mediating nerve growth

CC factor survival effect in melanocytic cells. p75NTR is a low affinity

CC nerve growth factor (NGF) receptor which is expressed by melanocytes and

CC keratinocytes of the basal epidermis. Apoptosis can be inhibited by

CC p75NTR via the upregulation of the Bcl-2 protein. These oligomer

CC sequences were used to determine that if p75NTR is occupied by

CC appropriate ligands e.g. neurotrophins, apoptosis is inhibited via

CC Bcl-2. Other examples of appropriate ligands include the cyclic peptides

CC AAY9233-Y39235, which are based on the beta-amyloid sequence, which

CC binds to p75NTR in Alzheimer's disease. The cyclic peptides can be used

CC in methods to control or manipulate keratinocyte or melanocyte cell

CC death. The methods involve using the peptides to bind as a pseudo-ligand

CC to the p75 neurotrophin receptor, inhibiting apoptosis. The new method

CC can induce or maintain hair growth, hair colour or skin colour. Inducing

CC or maintaining hair growth is useful for treating alopecia areata or

CC male pattern baldness in vertebrates.

XX
SQ Sequence 19 BP; 2 A; 9 C; 4 G; 4 T; 0 other;

Query Match 54.3%; Score 19; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 aagatgagcagctgg 32
|||||
DB 19 AAGATGGCGACGCTGG 1

Search completed: June 28, 2002, 22:40:02
Job time: 8078 sec

Mon Jul 1 08:40:53 2002

us-09-709-170a-2.szlm75.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:38 ; Search time 334.55 seconds
(without alignments)
25.698 Million cell updates/sec

Title: US-09-709-170A-2

Perfect score: 35

Sequence: 1 ctttcctctgggaagatgagcgcacgtgggaga 35

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/pdata1/1/ina/5A_COMB.seq:*
2: /cgn2_6/pdata1/1/ina/5B_COMB.seq:*
3: /cgn2_6/pdata1/1/ina/5A_COMB.seq:*
4: /cgn2_6/pdata1/1/ina/5B_COMB.seq:*
5: /cgn2_6/pdata1/1/ina/5A_COMB.seq:*
6: /cgn2_6/pdata1/1/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	35	100.0	35 1	US-08-217-082A-2
2	35	100.0	35 2	US-08-465-485A-2
3	35	100.0	35 3	US-09-080-285-2
4	20	57.1	20 1	US-08-217-082A-1
5	20	57.1	20 2	US-08-217-082A-7
6	20	57.1	20 2	US-08-465-485A-1
7	20	57.1	20 2	US-08-465-485A-7
8	20	57.1	20 3	US-09-080-285-1
9	20	57.1	20 3	US-09-080-285-7
10	20	57.1	20 4	US-09-379-718-1
11	20	57.1	20 4	US-09-379-718-2
12	18.6	53.1	27 1	US-08-410-804-13
13	18.6	53.1	27 1	US-08-607-269-8
14	18.6	53.1	27 1	US-08-559-514-13
15	18.6	53.1	27 2	US-08-858-311-13
16	18.6	53.1	27 5	PCT-US95-04600-8
17	18.6	53.1	18 1	US-08-217-082A-17
18	18.6	53.1	18 2	US-08-465-485A-17
19	18.6	53.1	18 3	US-08-465-485A-24
20	18.6	53.1	18 3	US-09-080-285-17
21	18.6	53.1	18 3	US-09-080-285-24
22	18.6	53.1	18 3	US-09-249-730-218
23	18.6	53.1	18 3	US-09-118-220-1
24	18.6	53.1	18 4	US-08-738-652-55
25	18.6	53.1	18 4	US-09-030-701-27
26	18.6	53.1	18 4	US-09-286-098-59
27	18.6	53.1	18 4	US-09-286-098-104

C 28	18	51.4	18 4	US-08-960-774-45	Sequence 45, Appl
C 29	18	51.4	18 4	US-09-078-954-14	Sequence 14, Appl
C 30	18	51.4	20 4	US-09-082-649B-60	Sequence 60, Appl
C 31	17	48.6	17 1	US-08-217-082A-9	Sequence 9, Appl
C 32	17	48.6	17 1	US-08-217-082A-10	Sequence 10, Appl
C 33	17	48.6	17 1	US-08-217-082A-11	Sequence 11, Appl
C 34	17	48.6	17 1	US-08-217-082A-12	Sequence 12, Appl
C 35	17	48.6	17 1	US-08-217-082A-13	Sequence 13, Appl
C 36	16.4	46.9	18 4	US-09-030-701-41	Sequence 41, Appl
C 37	16.4	46.9	18 4	US-09-030-701-60	Sequence 60, Appl
C 38	16.4	46.9	18 4	US-09-286-098-72	Sequence 72, Appl
C 39	16.4	46.9	18 4	US-08-960-774-72	Sequence 72, Appl
C 40	16.4	46.9	20 4	US-09-109-663-72	Sequence 72, Appl
C 41	15.8	45.1	40 1	US-08-231-342-12	Sequence 12, Appl
C 42	15.4	44.0	33 3	US-08-650-726-1	Sequence 1, Appl
C 43	15.4	44.0	70 1	US-08-434-001-109	Sequence 109, App
C 44	15.4	44.0	70 1	US-08-433-585-109	Sequence 109, App
C 45	15.4	44.0	70 1	US-08-434-425-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-08-217-082A-2
Sequence 2, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctttcctctggaagatgagcagctgggaga 35
|||||
Db 1 cttttcctctggaagatgagcagctgggaga 35

RESULT 2

US-08-465-485A-2
; Sequence 2, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-2

Query Match 100.0%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctttcctctggaagatgagcagctgggaga 35
|||||
Db 1 cttttcctctggaagatgagcagctgggaga 35

RESULT 3
US-09-080-285-2
; Sequence 2, Application US/09080285

; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-2

Query Match 100.0%; Score 35; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctttcctctggaagatgagcagctgggaga 35
|||||
Db 1 cttttcctctggaagatgagcagctgggaga 35

RESULT 4
US-08-217-082A-1/c
; Sequence 1, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; P.C.

STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-1

Query Match 57.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagagatggcgacgctg 30
|||||
DB 20 GGAAGAGATGGCGACGCTG 1

RESULT 5
US-08-217-082A-7
Sequence 7, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: NO
US-08-217-082A-7

Query Match 57.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagagatggcgacgctg 30
|||||
DB 1 GGAAGAGATGGCGACGCTG 20

RESULT 6
US-08-465-485A-1/c
Sequence 1, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-1

Query Match 57.1%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
|||||
Db 20 gggaagatgagcgacgctg 1

RESULT 7
US-08-465-485A-7
Sequence 7, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 57.1%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
|||||
Db 1 gggaagatgagcgacgctg 20

RESULT 8
US-09-080-285-1/c
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 57.1%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
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Db 20 gggaagatgagcgacgctg 1

RESULT 9
US-09-080-285-7
; Sequence 7, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-7

Query Match 57.1%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctg 30
|||||
Db 1 GGGAGGATGGCGACGCTG 20

RESULT 10
US-09-379-718-1/C
; Sequence 1, Application US/09379718
; Patent No. 6310047
; GENERAL INFORMATION:
; APPLICANT: Farrell, Nicholas
; APPLICANT: Kloster, Miriam

; TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
; FILE OF INVENTION: Antisense Technology
; FILE REFERENCE: farrell/kloster
; CURRENT APPLICATION NUMBER: US/09/379,718
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-379-718-1

Query Match 57.1%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctg 30
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Db 20 GGGAGGATGGCGACGCTG 1

RESULT 11
US-09-379-718-2
; Sequence 2, Application US/09379718
; Patent No. 6310047
; GENERAL INFORMATION:
; APPLICANT: Farrell, Nicholas
; APPLICANT: Kloster, Miriam
; TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
; FILE OF INVENTION: Antisense Technology
; FILE REFERENCE: farrell/kloster
; CURRENT APPLICATION NUMBER: US/09/379,718
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotides for gene therapy
; US-09-379-718-2

Query Match 57.1%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 gggaagatggcgacgctg 20

RESULT 12
US-08-410-804-13
; Sequence 13, Application US/08410804
; Patent No. 5632894
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cathryn Campbell
; STREET: 4370 La Jolla Village Drive, Ste 700
; CITY: San Diego
; STATE: California

COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-410-804-13

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 1 GGAATTCATGGCGACGCTGGAGA 25

RESULT 13
US-08-607-269-8
Sequence 8, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:
APPLICANT: Reed, John C.
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TITLE OF INVENTION: Interaction of Proteins Involved in a
CELL DEATH PATHWAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-607-269-8

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctggaga 35
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DB 1 GGAATTCATGGCGACGCTGGAGA 25

RESULT 14
US-08-259-514-13
Sequence 13, Application US/08259514
Patent No. 5747245
GENERAL INFORMATION:
APPLICANT: Reed, John C.
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,514
FILING DATE: 14-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-259-514-13

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 1 GGAATTCATGGCGACGCTGGAGA 25

RESULT 15

US-08-858-311-13
 ; Sequence 13, Application US/08858311
 ; Patent No. 5876939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Sato, Takaaki
 ; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cathryn Campbell
 ; STREET: 4370 La Jolla Village Drive, Ste 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/858,311
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/410,804
 ; FILING DATE: 27-MAR-1995
 ; APPLICATION NUMBER: US 08/259,514
 ; FILING DATE: 14-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 1389
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-858-311-13

Query Match 53.18; Score 18.6; DB 2; Length 27;
 Best Local Similarity 84.08; Pred. No. 16;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatgagcgacgctgggaga 35
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 Db 1 GGAATTCATGGCGACGCTGGGAGA 25

Search completed: June 28, 2002, 22:16:39
 Job time: 8265 sec

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C	42	12.2	61.0	57	9	AF084019	AF084019	Homo sapi
C	41	12.2	61.0	57	9	AF084014	AF084014	Homo sapi
C	40	12.2	61.0	57	9	AF084011	AF084011	Homo sapi
C	39	12.2	61.0	54	6	HSDFCRV13	HSDFCRV13	H. sapiens r
C	38	12.2	61.0	51	6	AX204060	AX204060	Sequence
C	37	12.2	61.0	50	6	191127	191127	Sequence 32
C	36	12.2	61.0	50	6	129453	129453	Sequence 32
C	35	12.2	61.0	50	6	AR032713	AR032713	Sequence
C	34	12.2	61.0	42	6	AX328775	AX328775	Sequence
C	33	12.2	61.0	34	6	AX037019	AX037019	Sequence
C	32	12.2	61.0	25	6	AX128282	AX128282	Sequence
C	31	12.2	61.0	24	6	169149	169149	Sequence 41
C	30	12.2	61.0	24	6	AX289570	AX289570	Sequence
C	29	12.2	61.0	21	6	AX113936	AX113936	Sequence
C	28	12.2	61.0	21	6	AX113935	AX113935	Sequence
C	27	12.2	61.0	20	6	AX294203	AX294203	Sequence
C	26	12.2	61.0	20	6	AR137423	AR137423	Sequence
C	25	12.4	62.0	24	6	AX291850	AX291850	Sequence
C	24	12.4	62.0	20	6	AX296483	AX296483	Sequence
C	23	12.6	63.0	75	6	AR035204	AR035204	Sequence
C	22	12.6	63.0	75	6	AR035203	AR035203	Sequence
C	21	12.6	63.0	51	6	AX116661	AX116661	Sequence
C	20	12.6	63.0	49	6	AX157798	AX157798	Sequence 10
C	19	12.6	63.0	47	6	A60797	A60797	Sequence
C	18	12.8	64.0	72	6	AX189915	AX189915	Sequence
C	17	12.8	64.0	51	6	AX189915	AX189915	Sequence
C	16	12.8	64.0	43	14	HSIDUP8	M12403	Hepes stimp
C	15	12.8	64.0	39	6	AR088564	AR088564	Sequence
C	14	12.8	64.0	39	6	AR088563	AR088563	Sequence
C	13	12.8	64.0	31	6	AX167323	AX167323	Sequence
C	12	12.8	64.0	31	6	AX092953	AX092953	Sequence
C	11	13	65.0	30	6	E07533	E07533	Oligonucleo
C	10	13	65.0	22	6	AR068325	AR068325	Sequence
C	9	13.2	66.0	51	6	AX165665	AX165665	Mus musculu
C	8	13.2	66.0	40	10	MUSRBBF	L35085	Mus musculu
C	7	13.4	66.0	31	6	AR098300	AR098300	Sequence
C	6	13.4	67.0	46	9	HSMLXID2	X96916	H. sapiens H
C	5	13.6	68.0	51	6	AX116165	AX116165	Sequence 4
C	4	20	100.0	33	6	196085	196085	Sequence
C	3	20	100.0	33	6	AR052606	AR052606	Sequence 3
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Best Local Similarity	100.0%;	Pred. No. 7.8;		

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
 LOCUS 196084 20 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 3 from patent US 5734033.
 ACCESSION 196084
 VERSION 196084.1 GI:3940554
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Reed,J.
 TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
 JOURNAL Patent: US 5734033-A 3 31-MAR-1998;
 FEATURES Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 7.8; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GATGCACCTACCCAGCCTCC 20

RESULT 3
 LOCUS AR052606 33 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5831066.
 ACCESSION AR052606
 VERSION AR052606.1 GI:5975970
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Reed,J.C.
 TITLE Regulation of bcl-2 gene expression
 JOURNAL Patent: US 5831066-A 4 03-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"
 BASE COUNT 5 a 5 c 16 g 7 t
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Query Match 100.0%; Score 20; DB 6; Length 33;
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 Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 4
 LOCUS 196085 33 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 4 from patent US 5734033.
 ACCESSION 196085
 VERSION 196085.1 GI:3940555

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Reed,J.
 TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
 JOURNAL Patent: US 5734033-A 4 31-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"
 BASE COUNT 5 a 5 c 16 g 7 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;

Query 1 gatgcacctaccagctcc 20
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 Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 5
 LOCUS AX116165 51 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 1288 from Patent WO0129262.
 ACCESSION AX116165
 VERSION AX116165.1 GI:14033107
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 51)
 AUTHORS Picoult-Newburg,L. and Pohl,M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 1288 26-APR-2001;
 FEATURES Location/Qualifiers
 source 1..51
 /organism="Homo sapiens"
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Query Match 68.0%; Score 13.6; DB 6; Length 51;
 Best Local Similarity 80.0%; Pred. No. 2.1e+04; Mismatches 4; Indels 0; Gaps 0;

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 Db 49 GATGCCCTCCCGCCTCC 30

RESULT 6
 LOCUS HSHLX1D2 46 bp DNA linear PRI 08-JAN-1997
 DEFINITION H.sapiens Hlx-1 gene, donor second intron.
 ACCESSION X96916
 VERSION X96916.1 GI:1770446
 KEYWORDS Hlx-1 gene; LIM 1 protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 46)
 AUTHORS Bozzl,F., Bertuzzi,S., Strina,D., Giannetto,C., Vezoni,P. and
 TITLE The exon-intron structure of human LHX1 gene
 JOURNAL Biochem. Biophys. Res. Commun. 229 (2), 494-497 (1996)

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Matches 14; Conservative	0;	Mismatches	1;							
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DB	32	TGCACCTACCCAGCC								
		linear								
		PAT 14-FEB-2001								

RESULT	7	31	12
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LOCUS	Sequence		
DEFINITION	AR098300		
ACCESSION	AR098300.1	GI:12807557	
VERSION			
KEYWORDS	unknown.		
SOURCE	unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 31)		
AUTHORS	Schiffman, J. Gregoire and de Leca, L.		
TITLE	Substituted, alpha-glycine acids that encode		
JOURNAL	Calculation, number 13 13 JUN-2000;		
FEATURES	Patent: US 6074872		
source	Location/Qualifiers		
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length 40:

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Best Local	Conservative	0;			
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OY	1	18			
	1 tccacctgccccagcgtcc				
Db				linear	

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RESULT 9
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LOCUS Sequence 860
DEFINITION AX165665 GI:14546494
ACCESSION AX165665.1
VERSION
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
          Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Mammalia; 1 (bases 1 to 51) and Leach.M.
          1 Shmleers, R.A. and containing single nucleotide polymorphisms and
          Nucleic acids thereof
          methods of use thereof 860 31-MAY-2001;
          Patent: WO 0138586-A (US)
          Curegen Corporation/Qualifiers
          Location/Qualifiers
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FEATURES
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[illegible]

RESULT 10 22 bp
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DEFINITION Sequence
AR068325
ACCESSION AR068325.1 GI:6000532
VERSION

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.s2lm75.rge

KEYWORDS
SOURCE Unknown
ORGANISM Unknown
REFERENCE Unclassified
AUTHORS 1 (bases 1 to 22)
TITLE Dille, B., Tan, X., Lundell, D., Lunn, C.A., Tan, J.C. and Zavadny, P.J.
JOURNAL Mammalian TMR-alpha convertases
FEATURES Patent: US 5853977-A 10/29-DEC-1998;
source location/Qualifiers
BASE COUNT 4 a 12 c 3 g 3 t
ORIGIN

Query Match
Best Local Similarity 65.0%; Score 13; DB 6; Length 22;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 cctaccagcctc 19
Db 8 cctaccagcctc 20

RESULT 11
LOCUS E07533/c
DEFINITION Oligonucleotide primer encoding the amino acid sequence included in
E07533
ACCESSION E07533
VERSION E07533.1 GI:2175668
KEYWORDS JP 1994141863-A/2;
SOURCE ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Morita, T. and Matsushiro, A.
TITLE MURINE GENE PARTIAL CLONING IN HOMOLOGOUS RECOMBINING REACTION
JOURNAL Patent: JP 1994141863-A 2 24-MAY-1994;
COMMENT MORITA TAKASHI, MATSUSHIRO AIZO
OS None
OC Artificial sequences.
FN JP 1994141863-A/2
PI 10-MAY-1994
PF 24-MAY-1994
PC MORITA TAKASHI, MATSUSHIRO AIZO
CC C12N15/12, C12N1/19//C12Q1/68;
CC strandness: Single;
FH key
FT Location: Linear;
FT source location/Qualifiers

FEATURES
source 1.30
location/Qualifiers
BASE COUNT 1.30
ORIGIN /db_xref="taxon:32644"
6 a 5 c 7 g 5 t 7 others

Query Match
Best Local Similarity 65.0%; Score 13; DB 6; Length 30;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 gctgacctaccagcctc 20
Db 22 gctgacctaccagcctc 20
RESULT 12
LOCUS AX092953
AX092953 31 bp DNA linear PAT 30-MAR-2001

DEFINITION Sequence 12 from Patent WO0118225.
ACCESSION AX092953
VERSION AX092953.1 GI:13509438
KEYWORDS
SOURCE ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 31)
AUTHORS Zhang, N.N.
TITLE Targeting constructs and transgenic animals produced therewith
JOURNAL Patent: WO 0118225-A 12/13-MAR-2001;
Xenogen Corporation (US);
FEATURES location/Qualifiers
source 1.31
/db_xref="taxon:32630"
/organism="synthetic construct"

BASE COUNT 9 a 10 c 9 g 3 t
ORIGIN /db_xref="taxon:32630"
/note="primer VNIP"

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 6; Length 31;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 atgcacctaccagc 17
Db 4 atgcacctaccagc 17
RESULT 13
LOCUS AX167323
DEFINITION Sequence 12 from Patent WO0144460.
ACCESSION AX167323
VERSION AX167323.1 GI:14596762
KEYWORDS
SOURCE ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 31)
AUTHORS Contag, P.R., Purcell, O.A.X. and Zhang, N.X.
TITLE Methods and compositions for screening for angiogenesis modulating
JOURNAL compounds
Patent: WO 0144460-A 12/21-JUN-2001;
Xenogen Corporation (US);
FEATURES location/Qualifiers
source 1.31
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/organism="synthetic construct"

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/note="primer VNIP"

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 6; Length 31;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 atgcacctaccagc 17
Db 4 atgcacctaccagc 17
RESULT 14
LOCUS AR088563/c
DEFINITION Sequence 12 from Patent US 5989899.
ACCESSION AR088563
VERSION AR088563.1 GI:10015327
KEYWORDS
SOURCE ORGANISM Unknown.
AR088563 39 bp DNA linear PAT 07-SEP-2000

Unclassified.
REFERENCE 1 /bacc 1 +

REFERENCE 1 (bases 1 to 39)

AUTHORS Bower, B.S., Clarkson, K.A., Larenas, E.A. and Ward, M.

TITLE Oversized cellulase compositions for use in detergent compositions

and in the treatment of textiles

JOURNAL Patent: US 5989899-A 12 23-NOV-1999;

FEATURES	Location/Qualifiers
COGNATE	LOCUS: 00 000000 N 12 E 20
ACCENT:	00 000000 N 12 E 20

FEATURES	LOCAL
SOURCE	1. .39

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source      L.: 39
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BASE COUNT	6 a	9 c	15 g	9 t
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BASE C
ORIGIN

Query Match	Score	DB	Length
64.0%	12.8	6	39

Best Local Similarity 87.5%; Pred. No. 5.8e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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4 gcaaccacccagccctc
| | | | | | | | | |
QY

Db 36 GGACCTACCCAGTCTC 21

RESULT 15

AR088564

LOCUS	AR088564	39 bp	DNA	linear	PAT 07-SEP-2000
-------	----------	-------	-----	--------	-----------------

LOCUS	AK000004	35 bp
DEFINITION	Sequence 13 from patent US 5989899.	

DEFINITION	SEQUENCE
ACCESSION	AR088564

ACCESSION	AR088564
VERSION	AR088564.1
	GI:10015328

KEYWORDS

KEYWORDS	SOURCE
.	Unknown.

SOURCE	Unknown.
ORGANISM	Unknown.

ORGANISM	Unknown. Unclassified.
1. <i>Staphylococcus aureus</i>	
2. <i>Staphylococcus epidermidis</i>	
3. <i>Staphylococcus saprophyticus</i>	
4. <i>Staphylococcus sciuri</i>	
5. <i>Staphylococcus carnosus</i>	
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7. <i>Staphylococcus aureus</i>	
8. <i>Staphylococcus aureus</i>	
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10. <i>Staphylococcus aureus</i>	
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98. <i>Staphylococcus aureus</i>	
99. <i>Staphylococcus aureus</i>	
100. <i>Staphylococcus aureus</i>	

REFERENCE 1 (bases 1 to 39)

REFERENCE	AUTHORS
1 (bases 1 to 39)	Bower, B.S., Clarkson, K.A., Larenas, E.A. and Ward, M.

AUTHORS	TITLE
Bower, B.S., Clarkson, K.A., Larenas, E.A. and Ward, M.	Oversized cellulase compositions for use in detergent compositions

TITLE
Oversized cellulase compositions
and in the treatment of textiles

and in the treatment of textiles
Patent: US 5989899-A 13 23-NOV-1999

JOURNAL Patent: US 5989899-A 13 23-N

FEATURES	Location
Source	1-30

source	1. .39
/organism="unknown"	

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BASE COUNT      9 a      15 c      9 t      6 +
                /organism="unknown"

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BASE C
ORIGIN

Query Match 64.08; Score 12.8; DB 6; Length 39

query match	64.0%;	score 12.8;	DB 6;	length 39;
Best Local Similarity	87.5%;	Pred. No. 5.8e+04;		

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Best Local Similarity 8/5%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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On 4 August 1998

QY 4 gcacctaccagccta

[illegible]

Search completed: June 28, 2002, 22:10:50
Job time: 8341 sec

Job time: 8341 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:02 ; Search time 1381.16 seconds

(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-3

Perfect score: 20

Sequence: 1 gatgcacctaccagcctcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAV19653	Human bcl-2 antisense
2	20	100.0	33	AAQ86646	Bcl-2 splice donor
3	20	100.0	33	AAV19654	Human bcl-2 oligon
4	14.2	71.0	26	AAZ57423	Oligonucleotide PC
5	14.2	71.0	47	AAZ68500	Human map-related
6	13.8	69.0	47	AAZ68807	Human map-related
7	13.6	68.0	51	AAH38492	Human SNP flanking
8	13.2	66.0	31	AAV09157	Preprocorristatin
9	13.2	66.0	41	AAI68122	Human growth hormo

c 10	13.2	66.0	41	22	AAI68123	Human growth hormo
c 11	13.2	66.0	51	22	AAI27169	Human SNP oligonuc
c 12	13.2	66.0	51	22	AAI31174	Human SNP oligonuc
c 13	13.2	66.0	51	22	AAI32505	Human SNP oligonuc
c 14	13.2	66.0	51	22	AAI32607	Human SNP oligonuc
c 15	13.2	66.0	51	22	AAI33975	Human SNP oligonuc
c 16	13.2	66.0	51	23	ABL00869	Human amino acid c
c 17	13	65.0	22	19	AAV20581	Human MT-MWP2 PCR
c 18	13	65.0	22	20	AAV73937	Human TNF-alpha co
c 19	13	65.0	30	15	AAQ64086	Rad51 primer. Syn
c 20	12.8	64.0	20	21	AAQ60942	Interleukin 10 sho
c 21	12.8	64.0	22	19	AAV41635	Nucleotide sequenc
c 22	12.8	64.0	22	21	AAA69535	PCR primer used to
c 23	12.8	64.0	31	22	AAH24936	PCR primer for mur
c 24	12.8	64.0	31	22	AAQ1053	Mouse 3'end vitron
c 25	12.8	64.0	31	24	AAQ22497	Mouse vitronectin
c 26	12.8	64.0	39	19	AAV44776	PCR primer for end
c 27	12.8	64.0	39	19	AAV44776	PCR primer for end
c 28	12.8	64.0	50	22	AAI33644	Human SNP oligonuc
c 29	12.8	64.0	51	22	AAH90214	Human clone c94402
c 30	12.8	64.0	72	16	AAQ91280	Exo-cellulohydrol
c 31	12.6	63.0	49	22	AAI74185	Human silent SNP c
c 32	12.6	63.0	51	22	AAI31094	Human SNP oligonuc
c 33	12.6	63.0	51	22	AAH38988	Human SNP flanking
c 34	12.6	63.0	75	13	AAQ30886	Primer 312-59. SY
c 35	12.6	63.0	75	13	AAQ30886	Primer 312-60. SY
c 36	12.4	62.0	17	19	AAV95263	Human c-fos target
c 37	12.4	62.0	20	24	AB196525	Capture oligonucle
c 38	12.4	62.0	24	24	AAI6083	Hybridised tagged
c 39	12.4	62.0	24	24	AB189620	Capture oligonucle
c 40	12.4	62.0	24	24	AB189621	Capture oligonucle
c 41	12.4	62.0	27	20	AAH33844	HBV probe G. Synt
c 42	12.4	62.0	30	9	AAH80762	Probe for detectio
c 43	12.4	62.0	30	10	AAH22223	Probe for HIV-1 VI
c 44	12.4	62.0	47	21	AAZ66889	Human map-related
c 45	12.2	61.0	20	21	AAZ95165	Primary forward PC

ALIGNMENTS

RESULT 1	
AAV19653	12-JUN-1998 (first entry)
AAV19653 standard; DNA; 20 BP.	
AAV19653:	
AC	AAV19653:
XX	
XX	
DT	12-JUN-1998 (first entry)
XX	
DE	Human bcl-2 antisense oligonucleotide 2.
XX	
KW	Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW	cancer; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	US5734033-A.
XX	
XX	
PD	31-MAR-1998.
XX	
PF	24-MAR-1994; 94US-0288692.
XX	
PR	21-FEB-1992; 92US-0840716.
PR	22-DEC-1988; 88US-0288692.
PR	24-MAR-1994; 94US-0217082.
XX	
PA	(TYPE-) UNIV PENNSYLVANIA.
XX	
PI	Reed J;
XX	
DR	WPI; 1998-229881/20.
XX	

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 6; Columns 3-4; 21pp; English.

CC This antisense oligonucleotide is complementary to the splice donor
CC site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are
CC phosphorothioate derivatives and can straddle strategic sites such as the
CC translation initiation site, donor and acceptor splicing sites, or sites
CC for transportation or degradation. Blocking translation at such strategic
CC sites prevents the formation of a functional bcl-2 gene product. These
CC oligonucleotides may be used for treating cancers associated with high
CC levels of bcl-2 gene expression, especially lymphomas and some
CC leukaemias.

XX Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 gatgcactaccagctcc 20

RESULT 2

AA086646/C
ID AA086646 standard; DNA; 33 BP.

XX AA086646;

XX 27-SEP-1995 (first entry)

DE Bcl-2 splice donor site.

XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;

OS Synthetic.

XX WO9508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US10725.

XX 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

XX WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

PS Disclosure; Page 13; 108pp; English.

XX The antisense oligonucleotide SD-AS (AA086645) is complementary to a
CC portion of the splice donor site of the pre-mRNA coding strand of the
CC human bcl-2 gene. It reduces the expression of bcl-2 gene product,
CC thereby inducing programmed cell death of certain cancer cells. The
CC corresp. bcl-2 sense splice donor site region was synthesized for use
CC as a control.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 3

AAV19654/C
ID AAV19654 standard; DNA; 33 BP.

XX AAV19654;

XX 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 2.

XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

XX Homo sapiens.

XX US5734033-A.

XX 31-MAR-1998.

XX 24-MAR-1994; 94US-0288692.

XX 21-FEB-1992; 92US-0840716.

XX 22-DEC-1988; 88US-0288692.

XX 24-MAR-1994; 94US-0217082.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

XX WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX Disclosure; Columns 3-4; 21pp; English.

CC This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the splice donor site of the human
CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 4

AAZ57423
ID AAZ57423 standard; DNA; 26 BP.

XX AAZ57423;

DT 07-APR-2000 (first entry)
XX
DE Oligonucleotide PCR primer pair #3 primer #1.
XX
KW PCR primer: Zaocys dhumnade; Tortoise plastron; Oviductus ranae;
KW discrimination: black snake; forest frog; oil; reagent box;
KW medicinal; ss.
XX
OS Synthetic.
XX
PN CN1232085-A.
XX
PD 20-OCT-1999.
XX
PF 31-MAR-1999; 99CN-0114133.
XX
PR 31-MAR-1999; 99CN-0114133.
XX
PA (UYNA-) UNIV NANJING.
XX
PI Wang Y, Zhou K, Liu Z;
XX
DR WPI: 2000-098492/09.
XX
PT Polymerase chain reaction (PCR) determining primer for Zaocys dhumnade,
PT Tortoise plastron and Oviductus ranae -
XX
PS Claim 1; Page 1; 4pp; Chinese.
XX
CC The present invention describes a special DNA sequence which can be used
CC to synthesise three pairs of high-specificity primers useful for
CC discriminating if black snake, tortoise plastron and forest frog oil are
CC true or false by simple polymerase chain reaction (PCR) of their DNA.
CC AA27419 to AA27424 represent specifically claimed primers from the
CC present invention. The primers can be used to make a reagent box for
CC discriminating medicinal materials with high speed and quality.
XX
SQ Sequence 26 BP; 6 A; 12 C; 1 G; 7 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatgcacctaccagctc 19
||| ||||| ||| |||||
DB 4 gatcactaacacaccc 22

RESULT 5
AA268500
ID AA268500 standard; DNA; 47 BP.
XX
AC AA268500;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:2847.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN W09954500-A2.
XX

PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
XX (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 3; Page 837; 2745pp; English.
XX
CC AA265654 to AA269578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 13 C; 10 G; 8 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatgcacctaccagctc 19
||||| ||||| ||||| |
DB 24 gatgcaactacacagccc 42

RESULT 6
AA268807/c
ID AA268807 standard; DNA; 47 BP.
XX
AC AA268807;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:3160.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN W09954500-A2.
XX
PD 28-OCT-1999.
XX

XX	21-APR-1999;	99WO-IB00822.
PF		
XX	21-APR-1998;	98US-0082614.
PR	23-NOV-1998;	98US-0109732.
XX		
XX	(GEST) GENSET.	
XX		
PI	Cohen D, Blumenfeld M, Chumakov I;	
XX		
DR	WPI; 2000-013267/01.	
XX		
XX	Novel biallelic markers used to construct a high density disequilibrium	
PT	map of the human genome	
XX		
PS	Claim 3; Page 904; 2745pp; English.	
XX		
CC	AA265654 to AA269578 represent human biallelic markers from the present	
CC	invention, which contain a polymorphic base at position 24 of their	
CC	nucleotide sequences. AA269579 to AA277440 represent amplification	
CC	primers for the biallelic markers. The biallelic markers of the	
CC	invention have a variety of uses: they can be used for high density	
CC	mapping of the human genome, and in complex association studies and	
CC	haplotyping studies which are useful in determining the genetic basis	
CC	for disease states. Compositions and methods of the invention can also	
CC	be useful for the identification of the targets for the development of	
CC	pharmaceutical agents and diagnostic methods, as well as the	
CC	characterisation of the differential efficacious responses to and side	
CC	effects from pharmaceutical agents acting on a disease as well as other	
CC	treatment.	
CC	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297	
CC	and 3367, are not actually given a sequence in the sequence listing	
CC	from the present invention.	
XX		
XX	Sequence 47 BP; 11 A; 11 C; 17 G; 8 T; 0 other;	
XX		

Query Match:	69.0%	Score 13.8:	DB 21:	Length 47:
Best local Similarity	88.2%	Pred. No. 2.4e+03:		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	4	gcacactaccagcctcc	20	
Db	46	GCAGCGACCCAGCCTCC	30	
RESULT 7				
AAH38492/c				
ID	AAH38492	standard; DNA; 51 BP.		
AC	AAH38492;			
XX				
DT	14-AUG-2001	(first entry)		
XX				
DE	Human SNP flanking oligonucleotide SPQ ID 1288.			
XX				
KW	Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNEP; genotyping; agammaglobulinemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; ds.			
KW				
XX				
OS	Homo sapiens.			
XX				
PN	WO200129262-A2.			
XX				
PN	26-APR-2001.			
XX				
PD				
XX				
XX	13-OCT-2000; 2000WO-US28436.			
PF				
XX				
XX	15-OCT-1999; 99US-0160096.			
PR				
XX				
XX				
DA	{ORCH-} ORCHID BIOSCIENCES INC.			

XX	PI	Picoault-Newburg L.	Pohl M;
XX	DR	WPI; 2001-290930/30.	
XX	PT	New genotyping oligonucleotide, useful for detecting the presence,	
XX	PT	absence or identity of single polynucleotide polymorphism in a nucleic	
XX	PT	acid sample	
XX	PS	Claim 1; Page 56; 83pp; English.	
XX	CC	Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide	
XX	CC	primer extension (SNEP) primers, and the sequences of regions flanking	
XX	CC	sites of single nucleotide polymorphisms SNPs. The present invention	
XX	CC	includes kits for determining the presence or absence of a SNP, using the	
XX	CC	oligonucleotides of the invention. The PCR primers are used to amplify a	
XX	CC	SNP flanking sequence, the SNPs primer is used as a genotyping primer.	
XX	CC	The oligonucleotides are useful for genotyping a nucleic acid sample by	
XX	CC	performing a single-nucleotide primer extension reaction. The	
XX	CC	oligonucleotides are useful for determining the presence, absence or	
XX	CC	identity of a SNP and for genotyping nucleic acid samples, for e.g. to	
XX	CC	assess by association analysis the genotype of an individual or group of	
XX	CC	individuals, having a pathological phenotypic trait suspected of being	
XX	CC	caused by one or more SNPs. Phenotypic traits include diseases e.g.	
XX	CC	agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular	
XX	CC	dystrophy, familial hypercholesterolemia, polycystic kidney disease,	
XX	CC	osteogenesis imperfecta and acute intermittent porphyria. Phenotypic	
XX	CC	traits also include symptoms of or susceptibility to multifactorial	
XX	CC	disease of which a component is or may be genetic such as autoimmune	
XX	CC	diseases, including, rheumatoid arthritis, multiple sclerosis,	
XX	CC	inflammation, cancer, nervous system diseases and infection by pathogenic	
XX	CC	microorganism. The method is also useful in forensic investigations and	
XX	CC	paternity analysis. The present sequence represents a fragment of human	
XX	CC	DNA flanking the site of a single nucleotide polymorphism.	
XX	SO	Sequence 51 BP; 9 A; 11 C; 24 G; 7 T; 0 other;	
QY		Query Match	68.0%; Score 13.6; DB 22; Length 51;
		Best Local Similarity	80.0%; Pred. No. 3e+03;
		Matches 16; Conservative	0; Mismatches 4; Indels 0; Gaps 0
		1 gatgcacctaccagcctcc 20	
DB		49 gatgcccccctccccgcctcc 30	
RESULT 8			
AAV09157/c			
ID	AAV09157	standard; cDNA; 31 BP.	
XX	AAV09157;		
XX	28-MAY-1998	(first entry)	
DE	Preprocortistatin 5' PCR primer 1.		
XX			
XX	Rat; mouse; human; preprocortistatin; N-terminal signal peptide;		
XX	procortistatin; cortistatin-29; cortistatin-14; agonist; antibody;		
XX	inhibition; sleep; somatostatin; neuronal electrical activity;		
XX	cerebral cortex; antagonist; acetylcholine; primer; PCR; immunoassay;		
XX	hybridisation; amplification; ss.		
XX	Synthetic.		
XX	WO9743417-A1.		
XX	20-NOV-1997.		
XX	15-MAY-1997;	97WO-US08481.	
XX	15-MAY-1996;	96US-0648322.	

PA (SCRI) SCRIPPS RES INST.
 XX De Lecea L, Henriksen SJ, Sigsgins GR, Sutcliffe JG;
 XX WPI; 1998-008886/01.
 DR
 XX
 PT New cortistatin peptide(s) - used to modulate sleep, detect
 PT mutation(s) and screen for drugs
 XX
 PS Claim 7; Page 107; 128pp; English.
 XX
 CC This is a 5' PCR primer used in the amplification of the novel
 CC preprocortistatin protein. Cleavage of the protein leads to the
 CC formation of procortistatin, which is processed to produce the mature
 CC cortistatin proteins referred as rat cortistatin-29, and cortistatin-14.
 CC The purified cortistatin, and its agonists, are used to induce sleep
 CC while its receptor antagonists (particularly antibodies) is used to
 CC inhibit sleep. Although cortistatin is structurally similar to
 CC somatostatin, it is able to depress neuronal electrical activity, induce
 CC low frequency waves in the cerebral cortex, antagonise acetylcholine and
 CC therefore enhance slow-wave sleep. The antibodies, and oligonucleotide
 CC primers, are used in usual immunoassays and hybridisation/amplification
 CC assays to detect or quantify cortistatin (including that administered
 CC therapeutically) or its nucleic acid. Oligonucleotides, e.g. antisense
 CC molecules, are used in vivo to alter cortistatin gene expression.
 CC Detection of a mutation in the cortistatin gene may provide diagnosis of
 CC sleep-related or neuronal depression-related disorders or diseases of
 CC the brain.
 XX
 SQ Sequence 31 BP; 8 A; 4 C; 13 G; 6 T; 0 other;
 XX
 Query Match 66.0%; Score 13.2; DB 19; Length 31;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 tgcacctaccacgacctcc 20
 ||||| ||||| |||||
 Db 30 TGCAGCCACCACCTCTCC 13
 RESULT 9
 AA168122/c
 ID AA168122 standard; DNA; 41 BP.
 XX
 AC AA168122;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 DE Human growth hormone family protein 9 probe 1.
 XX
 KW Human; growth hormone family protein 9; cytostatic; virucidal; HIV;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
 KW human immunodeficiency virus; infection; immunological disease;
 KW embryonic developmental disorder; growth disturbance;
 KW developmental disturbance; pregnancy abnormality; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200170809-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-CN00214.
 XX
 PR 07-MAR-2000; 2000CN-0111926.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-611485/70.
 XX

PT New protein 9 of growth hormone family and encoded polynucleotide,
 PT applicable in diagnosis and treatment of e.g. developmental disorders,
 PT tumour, haemopathy, human immunodeficiency virus infection, immunological
 PT diseases and inflammation
 XX
 PS Example 6; Page 15; 34pp; Chinese.
 XX
 CC The invention relates to human growth hormone family protein 9 with
 CC cyrostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
 CC activity. The polypeptide and encoded polynucleotide are applicable in
 CC diagnosis and treatment of malignant tumour, haemopathy, human
 CC immunodeficiency virus infection, immunological diseases and various
 CC inflammations, embryonic developmental disorders, growth disturbance,
 CC developmental disturbance and pregnancy abnormality. The present sequence
 CC is that of a probe, useful to the invention.
 XX
 SQ Sequence 41 BP; 9 A; 6 C; 20 G; 6 T; 0 other;
 XX
 Query Match 66.0%; Score 13.2; DB 22; Length 41;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 tgcacctaccacgacctcc 20
 ||||| ||||| |||||
 Db 29 TGCACCTAGCACCCTCC 12
 RESULT 10
 AA168123/c
 ID AA168123 standard; DNA; 41 BP.
 XX
 AC AA168123;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 DE Human growth hormone family protein 9 probe 2.
 XX
 KW Human; growth hormone family protein 9; cytostatic; virucidal; HIV;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
 KW human immunodeficiency virus; infection; immunological disease;
 KW embryonic developmental disorder; growth disturbance;
 KW developmental disturbance; pregnancy abnormality; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200170809-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-CN00214.
 XX
 PR 07-MAR-2000; 2000CN-0111926.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-611485/70.
 XX
 PD New protein 9 of growth hormone family and encoded polynucleotide,
 PT applicable in diagnosis and treatment of e.g. developmental disorders,
 PT tumour, haemopathy, human immunodeficiency virus infection, immunological
 PT diseases and inflammation
 XX
 PS Example 6; Page 15; 34pp; Chinese.
 XX
 CC The invention relates to human growth hormone family protein 9 with
 CC cyrostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
 CC activity. The polypeptide and encoded polynucleotide are applicable in
 CC diagnosis and treatment of malignant tumour, haemopathy, human
 CC immunodeficiency virus infection, immunological diseases and various
 CC inflammations, embryonic developmental disorders, growth disturbance,
 CC inflammations, embryonic developmental disorders, growth disturbance,

CC developmental disturbance and pregnancy abnormality. The present sequence
CC is that of a probe, useful to the invention.
XX
SQ Sequence 41 BP; 9 A; 6 C; 20 G; 6 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 41;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 tgcactaccagctcc 20
||||| |
DB 29 tgcacctaggcacctcc 12

RESULT 11
AAL27169/c
ID AAL27169 standard; DNA; 51 BP.
XX
AC AAL27169;
XX
DT 24-JAN-2002 (first entry)
XX

DE Human SNP oligonucleotide #377.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX

DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX

PS Claim 1; Page 1500; 4143pp; English.
XX

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX
SQ Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 atgcactaccagctcc 19
||||| |
DB 24 atgccatagccacgctcc 7

RESULT 12
AAL31174
ID AAL31174 standard; DNA; 51 BP.
XX
AC AAL31174;
XX
DT 24-JAN-2002 (first entry)
XX

DE Human SNP oligonucleotide #4382.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX

DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX

PS Claim 1; Page 2645; 4143pp; English.
XX

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 other;

	Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
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Db	47	ATGCCCATGCCAGCCTC	30							

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QY      3  tgcacctaccagctcc 20
          | | | | | | | | |
Db      2  ttcaagtcccaagctcc 19
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Job time: 8080 sec
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XX	AL33975;	
AC	AL33975;	
XX		
DF	24-JAN-2002	(first entry)
XX		
DE	Human SNP oligonucleotide #7183	

KM immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KM cyclin D polymerase; oncogene; histone; kinase; colony stimulating factor
 KM complement related protein; cytochrome; kinase; cytokine; interferon;
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M,

DR WPI; 2001-465210/50.

PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

PS Claim 1; Page 3448; 4143pp; English.

[illegible]

50 Sequence 51 BP; 8 A; 19 C; 12 G; 12 T; 0 other;

Query Match	66.0%;	Score 13.2;	DB 22;	Length 51;
Best Local Similarity	83.3%;	Pred. No. 4.7e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.szlm75.rng

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June 28, 2002, 22:16:39 ; Search time 534
(without alignments) updates/sec
14.684 Million cell

US-09-709-170A-3

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length: 0

Minimum DB seq length: 75	Match 0%
Maximum DB seq length: 100	Match 100%

post-processing
Maximum first 45
Listing
NA.*

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2: /cqgn2_6/ptodata/1/lma/6B_COMB.seq: *

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5: /cgn2-6/ptodata/1/lna/backfiles:1
6: /cgn2-6/ptodata/1/lna/backfiles:1

pred. no. greater than 0.5
score greater by analysts of
and is derived by

SUMMARIES

Desc

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      29      12.2      61.0
      30      12.2      61.0
      31      12.2      61.0
      32      12.2      61.0
      33      12.2      61.0
      34      12.2      61.0
      35      12.2      61.0
      36      12.2      61.0
      37      12.2      61.0
      38      12.2      60.0
      39      12.2      60.0
      40      12.2      60.0
      41      12.2      60.0
      42      12.2      60.0
      43      12.2      60.0
      44      12.2      60.0
      45      12.2      60.0

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ALIGNMENTS

Patent NO. 5,000,000
GENERAL INFORMATION: Antisense oligonucleotides
Inventor: Reed, John
Agent: [redacted] Cells expressing the

APPLICANT: GROWTH OF
TITLE OF INVENTION: 17
OF INVENTION: WATER & NEUSTADT

TITLE OF SEQUENCES:
NUMBER OF ADDRESSES:
RESPONSE ADDRESS: SPIYAK, MCCLELLAND,

CORRESPONDENCE: OBLON,
ADDRESSEE: P.C.
ADDRESSEE: Airport Parkway

ADDRESS: 224 ALF-
STREET: San Jose
CITY: California

CITY: Calliope
STATE: U.S.A.
COUNTRY: U.S.A.

COOR: 95110
ZIP: 95110
COMPUTER READABLE FORM: disk
FLOPPY disk

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COMPUTER TYPE: IBM PC compatible version #1.23
MEDIUM: PC-DOS/MS-DOS
SYSTEM: PC-DOS/MS-DOS #1.0, release
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OPERATING system kernel
OPERATING patent in Korea
SOFTWARE: communication DATA:
US/08/217,082A

CURRENT APPLICATION NUMBER: 02/00000000
 CURRENT APPLICATION NUMBER: 02/00000000
 APPLICATION NUMBER: 02/00000000
 DATE: 24-MAR-1994

FILING DATE: 433
 CLASSIFICATION DATA: NS 07/840,716
 CLASSIFICATION DATA:

PRIOR APPLICATION NUMBER: 22
APPLICATION DATE: 21-FEB-1992
DATA: 692

FILING DATE: US 07/286,000
PRIORITY NUMBER: 07/286,000
PRIORITY DATE: DEC-1988

APPLICANT: 22-DEC
FILING DATE: INFORMATION:
REVIEW AGENT: Andrew D. COO

ATTORNEY, NAME: Fortney, Andrew
REGISTRATION NUMBER: 34,800
REGISTRATION NUMBER: 3335-067-55 EMO

REGISTRATION INFORMATION:
REFERENCE INFORMATION: 436-2070
COMMUNICATIONS: (408) 436-2070

TELEPHONE: (408) 436-2075
TELEFAX: (408) 436-2075
ID NO: 3

TELETYPE FOR SEX INFORMATION CHARACTERISTICS:
SCIENCE base pairs

SEQUENCE: 20 base
LENGTH: nucleic acid
TYPE: single

STRANDEDNESS: linear
TOPOLOGY: other nucleic acid
DNA

MOLECULE TYPE: Synthetic
DESCRIPTION: YES

ANTI-SENSE:
00-217-082A-3

US-00

100

1

1

Page 1

Mon Jul 1 08:40:54 2002

us-09-709-1702-3.s21m75.rn1

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gatgcacctaccagctcc 20
Db 1 gatgcacctaccagctcc 20

RESULT 2
US-08-465-485A-3
Sequence 3, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/465,485A
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 21-FEB-1992
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: US 07/288,692
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION: 3335-070-55 CONT
TELEPHONE: (408) 436-2070
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gatgcacctaccagctcc 20
Db 1 gatgcacctaccagctcc 20
RESULT 3
US-09-080-285-3

Sequence 3, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/09/080,285
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 21-FEB-1992
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: US 07/288,692
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION: 3335-070-55 CONT
TELEPHONE: (408) 436-2070
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gatgcacctaccagctcc 20
Db 1 gatgcacctaccagctcc 20
RESULT 4
US-08-217-082A-4/c
Sequence 4, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/217,082A
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 21-FEB-1992
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: US 07/288,692
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION: 3335-070-55 CONT
TELEPHONE: (408) 436-2070
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-217-082A-4/c

ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-4

Query Match 100.0%; Score 20; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgacctaccagctcc 20
|||||
Db 29 GATGACCTACCAGCTCC 10

RESULT 5
US-08-465-485A-4/C
Sequence 4, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-4

Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgacctaccagctcc 20
|||||
Db 29 GATGACCTACCAGCTCC 10

RESULT 6
US-09-080-285-4/C
Sequence 4, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-4

Query Match 100.0%; Score 20; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gatgcacctaccagctcc 20
|||||
Db 29 GATGCACCTACCAGCTCC 10

RESULT 7
US-08-648-322-13/C
Sequence 13, Application US/08648322
Patent No. 6074872
GENERAL INFORMATION:
APPLICANT: Sutcliffe, Gregor J.
APPLICANT: de Lecea, Luis
TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. 6074872th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,322
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 519.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-648-322-13

Query Match 66.0%; Score 13.2; DB 3; Length 31;

Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 3 tgcacctaccagctcc 20
|||||
Db 30 TGCAGCCACCACCTCC 13

RESULT 8
US-08-889-909A-10
Sequence 10, Application US/08889909A
Patent No. 5853977
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles
APPLICANT: Tan, Jimmy
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Mammalian TNF- α Convertases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,909A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,710
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, No. 5853977man C.
REGISTRATION NUMBER: 31,608
REFERENCE/DOCKET NUMBER: JB0601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2906
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-889-909A-10

Query Match 65.0%; Score 13; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 octaccagctcc 19
|||||
Db 8 CCAACCCAGCCTC 20

RESULT 9
US-09-156-163A-10
Sequence 10, Application US/09156163A
Patent No. 6319681
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong

APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles
APPLICANT: Tan, Jimmy
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Mammalian TNF-a Convertases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Gallopping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 8.1
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/156,163A
FILING DATE: 9/17/98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/889,909
FILING DATE: July 10, 1997
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: McLaughlin, Jaye P.
REGISTRATION NUMBER: 41,211
REFERENCE/DOCKET NUMBER: J86010B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 5056
TELEFAX: 908 298 5388
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-156-163A-10

Query Match 65.0%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 cctaccagctc 19
|||||

Db 8 CCACTACCAAGCTC 20

RESULT 10
US-08-646-538-32
Sequence 32, Application US/08646538
Patent No. 602781
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 602781 yet assigned
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note="oligonucleotide #18990"
US-08-646-538-32

Query Match 64.0%; Score 12.8; DB 3; Length 26;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagctcc 20
|||

Db 9 CAGTATCAGAGCTCC 24

RESULT 11
US-09-503-222-32
Sequence 32, Application US/09503222
Patent No. 6265548
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note="oligonucleotide #18990"
US-09-503-222-32

Query Match 64.0%; Score 12.8; DB 4; Length 26;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagcctcc 20
||| || |||||
Db 9 CACGTATCCAGCCTCC 24

RESULT 12
US-08-646-538-33/C
Sequence 33, Application US/08646538
Patent No. 6027881
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
NUMBER OF SEQUENCES: 37
PROTEINS HAVING INCREASED CELLULAR FLUORESCENCE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 6027881 yet assigned
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..28
OTHER INFORMATION: /note="oligonucleotide #18991"
US-08-646-538-33

Query Match 64.0%; Score 12.8; DB 3; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagcctcc 20
||| || |||||
Db 16 CACGTATCCAGCCTCC 1

RESULT 13
US-09-503-222-33/C
Sequence 33, Application US/09503222
Patent No. 6265548
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
NUMBER OF SEQUENCES: 37
PROTEINS HAVING INCREASED CELLULAR FLUORESCENCE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..28
OTHER INFORMATION: /note="oligonucleotide #18991"
US-09-503-222-33

Query Match 64.0%; Score 12.8; DB 4; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagcctcc 20
||| || |||||
Db 16 CACGTATCCAGCCTCC 1

RESULT 14

STATE: CALIFORNIA

Search completed: June 28, 2002, 22:16:40
Job time: 8266 sec

Search completed: June 28, 2002, 22:16:40
Job time: 8266 sec

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.szlm75.rni

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:50 ; Search time 3762.88 Seconds
(without alignments)
183.523 Million cell updates/sec

Title: US-09-709-170A-4

Perfect score: 33
Sequence: 1 acgggagcagagcgtggtcagtgatcctcgtc 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
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8: gb_pl: *
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11: gb_sts: *
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13: gb_un: *
14: gb_vi: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_ov: *
22: em_or: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlgc_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	33	100.0	33	6	AR052606	Sequence 196085
2	33	100.0	33	6	AR052605	Sequence 196084
3	20	60.6	20	6	AR129866	Sequence AR129866
4	20	60.6	20	6	AR156905	Sequence AR156905
5	17.6	53.3	40	6	AR156905	Sequence AR156905
6	17.6	53.3	40	6	AR156905	Sequence AR156905
7	16.6	50.3	66	6	AR038054	Sequence AR038054
8	16.2	49.1	59	23	AR038054	Sequence AR038054
9	16.2	49.1	59	23	AR038054	Sequence AR038054
10	15.6	47.3	51	6	AR044319	Sequence AR044319
11	15.4	46.7	36	6	AR044319	Sequence AR044319
12	15.4	46.7	36	6	AR044319	Sequence AR044319
13	15.4	46.7	36	6	AR044319	Sequence AR044319
14	15.4	46.7	36	6	AR044319	Sequence AR044319
15	15.4	46.7	36	6	AR044319	Sequence AR044319
16	14.8	44.8	52	6	AR098300	Sequence AR098300
17	14.6	44.2	31	6	AR098300	Sequence AR098300
18	14.6	44.2	31	6	AR098300	Sequence AR098300
19	14.6	44.2	31	6	AR098300	Sequence AR098300
20	14.6	44.2	31	6	AR098300	Sequence AR098300
21	14.6	44.2	31	6	AR098300	Sequence AR098300
22	14.4	43.6	48	6	AR117049	Sequence AR117049
23	14.4	43.6	48	6	AR117049	Sequence AR117049
24	14.4	43.6	48	6	AR117049	Sequence AR117049
25	14.4	43.6	48	6	AR117049	Sequence AR117049
26	14.4	43.6	48	6	AR117049	Sequence AR117049
27	14.4	43.6	48	6	AR117049	Sequence AR117049
28	14.4	43.6	48	6	AR117049	Sequence AR117049
29	14.4	43.6	48	6	AR117049	Sequence AR117049
30	14.4	43.6	48	6	AR117049	Sequence AR117049
31	14.2	43.0	51	6	AR0204020	Sequence AR0204020
32	14.2	43.0	51	6	AR0204020	Sequence AR0204020
33	14.2	43.0	51	6	AR0204020	Sequence AR0204020
34	14.2	43.0	51	6	AR0204020	Sequence AR0204020
35	14.2	43.0	51	6	AR0204020	Sequence AR0204020
36	14.2	43.0	51	6	AR0204020	Sequence AR0204020
37	14.2	43.0	51	6	AR0204020	Sequence AR0204020
38	14.2	43.0	51	6	AR0204020	Sequence AR0204020
39	14.2	43.0	51	6	AR0204020	Sequence AR0204020
40	13.8	41.8	26	8	AR090965	Sequence AR090965
41	13.8	41.8	26	8	AR090965	Sequence AR090965
42	13.8	41.8	26	8	AR090965	Sequence AR090965
43	13.8	41.8	26	8	AR090965	Sequence AR090965
44	13.8	41.8	26	8	AR090965	Sequence AR090965
45	13.8	41.8	26	8	AR090965	Sequence AR090965

ALIGNMENTS

RESULT 1	AR052606	33 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR052606				
DEFINITION	Sequence 4 from patent US 5831066.				
ACCESSION	AR052606				
VERSION	AR052606.1	GI:5975970			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 33)				
AUTHORS	Reed, J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 03-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..33				
BASE COUNT	5 a 5 c 10 g 7 t				
ORIGIN					

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0024;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcacatctgt 33
|||||
Db 1 ACGGGCTACGGAGCTGGGTAGTGCATCTGCT 33

RESULT 2
196085 196085 33 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 4 from patent US 5734033.
DEFINITION
ACCESSION 196085 GI:3940555
VERSION 196085.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 4 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 5 a 5 c 16 g 7 t
ORIGIN

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcacatctgt 33
|||||
Db 1 ACGGGCTACGGAGCTGGGTAGTGCATCTGCT 33

RESULT 3
AR052605/c AR052605 20 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5831066.
DEFINITION
ACCESSION AR052605
VERSION AR052605.1 GI:5975969
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 3 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 10 c 3 g 3 t
ORIGIN

Query Match 60.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ggaggtggtgtagtcacatc 29
|||||
Db 20 GGAGGCTGGGTAGTGCATC 1

RESULT 4
196084/c 196084 20 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 3 from patent US 5734033.
DEFINITION
ACCESSION 196084
VERSION 196084.1 GI:3940554

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 3 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 10 c 3 g 3 t
ORIGIN

Query Match 60.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ggaggtggtgtagtcacatc 29
|||||
Db 20 GGAGGCTGGGTAGTGCATC 1

RESULT 5
AR129866/c AR129866 40 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 16 from patent US 6187564.
DEFINITION
ACCESSION AR129866
VERSION AR129866.1 GI:14117763
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Sytkowski,A.J.
TITLE DNA encoding erythropoietin multimers having modified 5' and 3' sequences and its use to prepare EPO therapeutics
JOURNAL Patent: US 6187564-A 16 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"

BASE COUNT 5 a 19 c 9 g 7 t
ORIGIN

Query Match 53.3%; Score 17.6; DB 6; Length 40;
Best Local Similarity 71.9%; Pred. No. 7.4e+03;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcacatctgt 32
|||||
Db 32 ACAGGGGACAGACCGCGGTGTGATCTGG 1

RESULT 6
AR156905/c AR156905 40 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 4 from patent US 6242570.
DEFINITION
ACCESSION AR156905
VERSION AR156905.1 GI:15125609
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Sytkowski,A.J.
TITLE Production and use of recombinant protein multimers with increased biological activity
JOURNAL Patent: US 6242570-A 4 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"

[illegible]

LOCUS	57 bp	DNA	linear	PAT 01-SEP-2000
DEFINITION	Sequence 7 from patent US 5975551.			
ACCESSION	AB082754			

VERSION AR082754.1 GI:10009544

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 57)

AUTHORS Motez,E., Abastado,J. and Kourilsky,P.

TITLE Altered major histocompatibility complex (MHC) determinant and

JOURNAL Patent: US 5976551-A 7 02-NOV-1999;

FEATURES Location/Qualifiers

SOURCE 1..57

BASE COUNT 8 a 12 c 28 g 9 t

ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 57;

Best Local Similarity 67.7%; Pred. No. 8.9e+04; Mismatches 10; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 ggggtacggagcgtggtagtgatctggt 33

DB 9 GGGGATCGATCCGAGCGGATCGATCCGAT 39

RESULT 15

AR119736 AR119736 57 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6153408.

ACCESSION AR119736

VERSION AR119736.1 GI:14102435

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 57)

AUTHORS Abastado,J., Motez,E., Kourilsky,P., Casrouge,A., Ojcius,D. and

Lone,Y.

TITLE Altered major histocompatibility complex (MHC) determinant and

JOURNAL Patent: US 6153408-A 7 28-NOV-2000;

FEATURES Location/Qualifiers

SOURCE 1..57

BASE COUNT 8 a 12 c 28 g 9 t

ORIGIN

Query Match 45.5%; Score 15; DB 6; Length 57;

Best Local Similarity 67.7%; Pred. No. 8.9e+04; Mismatches 10; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 ggggtacggagcgtggtagtgatctggt 33

DB 9 GGGGATCGATCCGAGCGGATCGATCCGAT 39

Search completed: June 28, 2002, 22:10:53
Job time: 8344 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:04 ; Search time 1361.16 Seconds
(without alignments)
41.022 Million cell updates/sec

Title: US-09-709-170A-4

Perfect score: 1
Sequence: 1 acgggagcagagcgtggtgagtcattcgtt 33

Scoring table:
IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	33	16	AA086646
2	33	100.0	33	19	AAV19654
3	20	60.6	20	19	AAV19653
4	18.2	55.2	47	21	AA268500
5	17.6	53.3	35	18	AAV79533
6	17.6	53.3	40	20	AA25704
7	16.6	50.3	50	21	AAV76605
8	16.2	49.1	45	21	AAA05784
9	16.2	49.1	51	22	AA134288

ALIGNMENTS

RESULT	ID	AA086646	standard; DNA; 33 BP.
AC	AA086646:		
DT	27-SEP-1995	(first entry)	
DE	Bcl-2 splice donor site.		
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;		
KW	leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;		
KW	ss.		
OS	Synthetic.		
PN	W09508350-A.		
XX	30-MAR-1995.		
XX	20-SEP-1994;	94WO-US10725.	
XX	20-SEP-1993;	93US-0124256.	
XX	(REED/) REED J C.		
XX	Reed JC;		
XX	WPI, 1995-139394/18.		
XX	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment		
XX	of human solid tumours, esp. breast cancer		

Trypsin-like enzyme
Synthetic gene shM
Synthetic gene shM
Oligonucleotide PC
Human SNP oligonuc
Human SNP flanking
Rad51 primer. Syn
Human SNP oligonuc
Spacer SC-15 Syn
Human caveolin pro
Quadruplex/duplex
Quadruplex/duplex
Oligonucleotide SP
Preprocrystatin
Human VEGF-B167 ma
probe for progenit
Human SNP oligonuc
Human SNP flanking
Human SNP flanking
Primer for Human o
Exo-cellulohydroxyl
HLA type analysis
Human FEN-1 DNA fr
A. thaliana dihydr
Repetitive protein
Oligonucleotide us
Oligonucleotide us
HPV primer probe H
Human SNP oligonuc
Human clone c94402
Human amino acid c
DNA sequence of pr
Primer for amplifi
Human protective D
Polymorphic fragme

XX Disclosure: Page 13; 108bp; English.

CC The antisense oligonucleotide SD-AS (AA086645) is complementary to a
CC portion of the splice donor site of the pre-mRNA coding strand of the
CC human bcl-2 gene. It reduces the expression of bcl-2 gene product,
CC thereby inducing programmed cell death of certain cancer cells. The
CC corresp. bcl-2 sense splice donor site region was synthesized for use
CC as a control.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 33; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acggggtacggagctgtgtagtgcattcgt 33
DB 1 acggggtacggagctgtgtagtgcattcgt 33

RESULT 2

AAV19654
ID AAV19654 standard; DNA; 33 BP.

AC AAV19654;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 2.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Disclosure; Columns 3-4; 21pp; English.

CC This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the splice donor site of the human
CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match

100.0%; Score 33; DB 19; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acggggtacggagctgtgtagtgcattcgt 33
DB 1 acggggtacggagctgtgtagtgcattcgt 33

RESULT 3

AAV19653/C
ID AAV19653 standard; DNA; 20 BP.

AC AAV19653;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 antisense oligonucleotide 2.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 6; Columns 3-4; 21pp; English.

CC This antisense oligonucleotide is complementary to the splice donor
CC site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are
CC phosphorothioate derivatives and can straddle strategic sites such as the
CC translation initiation site, donor and acceptor splicing sites, or sites
CC for transportation or degradation. Blocking translation at such strategic
CC sites prevents the formation of a functional bcl-2 gene product. These
CC oligonucleotides may be used for treating cancers associated with high
CC levels of bcl-2 gene expression, especially lymphomas and some
CC leukaemias.

XX Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 other;

Query Match

Best Local Similarity 60.6%; Score 20; DB 19; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ggaagctggtagtgcattc 29
DB 20 GGAGCTGGTAGTGCATC 1

RESULT 4

AAZ68500/C
ID AAZ68500 standard; DNA; 47 BP.

AC AAZ68500;

XX

DT		10-SEP-2001	(first entry)
XX			
DE	Human map-related biallelic marker SEQ ID NO:2847.		
KW	Human genome; biallelic marker; high density disequilibrium map;		
KW	genomic map; haplotype; phenotype; polymorphic base; genotyping;		
KM	haplotyping; hybridisation; identification; characterisation;		
KM	diagnosis; single nucleotide polymorphism; SNP; ds.		
XX			
OS	Homo sapiens.		
XH			
XX	Key	Location/Qualifiers	
FT	variation	replace(24,C)	
FT		/tag= a	
FT		/standard_name= "single nucleotide polymorphism"	
EN	W09954500-A2.		
XX			
PD	28-OCT-1999.		
XX			
PF	21-APR-1999;	99WO-IB00822.	
XX			
PR	21-APR-1998;	98US-0082614.	
PR	23-NOV-1998;	98US-0109732.	
PA	(GEST) GENSET.		
PI	Cohen D, Blumenfeld M, Chumakov I;		
XX			
DR	WPI; 2000-013267/01.		
XX			
PT	Novel biallelic markers used to construct a high density disequilibrium		
PS	map of the human genome -		
XX			
XX	Claim 3; Page 837; 2745pp; English.		
CC	AA265654 to AA269578 represent human biallelic markers from the present		
CC	Invention, which contain a polymorphic base at position 24 of their		
CC	nucleotide sequences. AA269579 to AA277440 represent amplification		
CC	primers for the biallelic markers. The biallelic markers of the		
CC	Invention have a variety of uses: they can be used for high density		
CC	mapping of the human genome, and in complex association studies and		
CC	haplotyping studies which are useful in determining the genetic basis		
CC	for disease states. Compositions and methods of the invention can also		
CC	be useful for the identification of the targets for the development of		
CC	pharmaceutical agents and diagnostic methods, as well as the		
CC	characterisation of the differential efficacious responses to and side		
CC	effects from pharmaceutical agents acting on a disease as well as other		
CC	treatment.		
CC	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297		
CC	and 3367, are not actually given a sequence in the Sequence Listing		
CC	from the present Invention.		
XX			
SQ	Sequence 47 BP; 16 A; 13 C; 10 G; 8 T; 0 other;		
OY	Query Match	55.2%; Score 18.2; DB 21; Length 47;	
	Best Local Similarity	87.0%; Pred. No. 3.4e+02;	
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	11 gagctgggtagtcacatcgtg 33		
DB	42 GGGCGTGTGTAGTTGCATCTGCT 20		
RESULT	5		
ID	AAAT79533		
XX	AAAT79533 standard; DNA; 35 BP.		
AC	AAAT79533;		
XX			
DT	06-MAR-1998 (first entry)		
XX			

DE	Fos	leucine zipper FR618.
XX		
KM	Protein-protein interaction; interacting polypeptide;	
KM	polypeptide principle; Fos; transcription factor; PCR; primer; ss.	
XX		
OS	Synthetic.	
XX		
PN	WC9732017-A1.	
PD		
04-SEP-1997.		
XX		
PF	26-FEB-1997; 97WO-EP00931.	
XX		
PR	26-FEB-1996; 96EP-0102852.	
XX		
PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
XX		
P1	Ge L, Ilaq V;	
XX		
DR	WPI; 1997-448687/41.	
XX		
PT	Identification of interacting polypeptide encoding nucleic acid sequences - e.g. to identify protein-protein interactions, which play an important role in biological processes	
PT		
XX		
PS	Example 6; Page 41; 105pp; English.	
XX		
CC	Primers FR618 (AAT79533) and FR619 (AAT79534) were used in the PCR amplification of DNA encoding the leucine zipper domain of fos	
CC	transcription factor. The PCR product was used to create vector pUC18-IMFfos. This was used in a novel method of identifying	
CC	nucleic acid sequences that encode interacting peptides or proteins. The method involves generating 2 libraries of recombinant vectors, expressing members of the libraries in host cells so that at least one interaction is established, and selecting for the generation of a screenable or selectable	
CC	property representing the interaction of polypeptides. pUC18-IMFfos was used in an experiment to demonstrate selectively	
CC	infective phage (SIP)-based library versus library screening via in vitro recombination of separately constructed libraries into one phase vector. In this case, the cognate pairing is from the interaction between jun and fos.	
CC		
SO	Sequence 35 BP; 1 A; 9 C; 16 G; 9 T; 0 other:	
XX		
Query Match	53.3%; Score 17.6; DB 18; Length 35;	
Best Local Similarity	71.9%; Pred. No. 5.8e+02;	
Matches 23; Conservative	0; Mismatches 9; Indels 0; Gaps	
QY	2 cggggtacgagcgtctggtgcgtcatctgtt 33 Db 1 cgccgtacgcgcgtctcgtagtggttcgtg 32	
RESULT 6		
AAX25704/C		
ID AAX25704 standard; DNA: 40 BP.		
XX		
AC AAX25704;		
XX		
DT 21-MAY-1999 (first entry)		
XX		
DE Human erythropoietin homodimer fusion gene primer Epa3-3.		
XX		
KM Human; erythropoietin; dimer; trimer; polymer; fusion protein; cancer		
KM biological activity; anemia; proliferation; differentiation; ss;		
KM progenitor; leucocyte; granulocyte; blood; myelosuppressed patient;		
XX		
primer; PCR; amplification.		
XX		
OS Synthetic.		
OS Homo sapiens.		
XX		

XX (TEIJ) TEIJUN LTD.
XX Masuda K, Ogawa H, Suga T, Sugimoto Y, Takagi K,
PI Yamacka K, Yasuoka S,
XX WPI: 1996-117356/13.
XX
XX Nucleic acid sequence encoding trypsin-like enzyme - which digests
PT fibrinogen, used as expectorant in treatment of respiratory
PT diseases, e.g. bronchial asthma
XX
XX Example 9; Page 43; 65pp; English.
XX
XX Example 9 describes the cloning of cDNA region encoding
CC trypsin-like enzyme isolated from cough phlegm.
CC Four oligonucleotides are used for PCR: TRY-1 (AAT10694), TRY-8
CC (AAT10695), TRY-10 (AAT10696) and TRY-11 (AAT10697).
CC TRY-1 corresponds to from A1 to A23 of the sequence given in
CC AAT10693, which is part of a cDNA encoding the trypsin-like
CC enzyme. TRY-8 corresponds to from G16 to T40 of AAT10693.
CC TRY-10 is capable of annealing to the 3'-terminus of poly(A)+ RNA.
CC TRY-11 is identical to the 5'-terminus side 19 residues of TRY-10.
CC After amplification, plasmid p19-33 was obtained. p19-33 encodes
CC part of the N-terminus amino acid sequence 20 residues of the
CC trypsin-like enzyme isolated from the cough phlegm (see AAT10698).
XX
XX Sequence 59 BP; 11 A; 12 C; 26 G; 10 T; 0 other;
XX

Query Match 49.1%; Score 16.2; DB 17; Length 59;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ggggtacggagcgtggtgtagg 23
||| ||||| ||| |||
DB 8 ggggcacggagcgtggtgtagg 28

RESULT 11
AAS04737/c
ID AAS04737 standard; DNA; 66 BP.
XX
XX AAS04737;
XX
XX 07-SEP-2001 (first entry)
XX
XX Synthetic gene shMOBP/MS, PCR primer #4.
XX
XX shMOBP/MS: PCR primer; ss; immunogenic epitope cluster; IEC;
KW synthetic human myelin-oligodendrocytic basic protein; autoantigen;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;
KW autoimmune hepatitis; thyroiditis; orchitis;
KW idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX W0200131037-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-IL00688.
XX
XX 27-OCT-1999; 99IL-0132611.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Ben-Nun A, Kerlero De Rosbo N, Sappler GP;
PI
XX WPI: 2001-300515/31.
XX
XX

XX Novel synthetic human target autoantigen gene useful for treating
PT autoimmune diseases such as multiple sclerosis, insulin-dependent
PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis
PT
XX
XX Example 5; Fig 26; 182pp; English.
XX
XX The sequence is a PCR primer used in the construction of a nucleic acid
CC encoding shMOBP/MS (synthetic human myelin-oligodendrocytic
CC basic protein containing immunogenic epitope clusters (IEC) from MOBP.
CC The synthetic human target autoantigen genes of the invention comprise
CC sequences coding for at least 2 IECs of autoantigen(s) related to a
CC specific autoimmune disease. The synthetic human target autoantigen genes
CC are useful for treating autoimmune diseases such as multiple sclerosis,
CC insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia
CC gravis, uveitis, autoimmune hepatitis, thyroiditis, orchitis,
CC idiopathic thrombocytopenic purpura, and inflammatory diseases (Crohn's
CC disease, ulcerative colitis). The synthetic human target autoantigen
CC genes are also useful for diagnosis and/or monitoring the progression of
CC the autoimmune disease.
XX
XX Sequence 66 BP; 17 A; 28 C; 15 G; 6 T; 0 other;
XX

Query Match 48.5%; Score 16; DB 22; Length 66;
Best Local Similarity 68.8%; Pred. No. 2.6e+03;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 acgggtacggagcgtggtgtaggtagcctgg 32
||| ||||| ||||| ||| ||| |||
DB 40 ACTTGACACGGCGGCTGTGTACGGGCTTCTGG 9

RESULT 12
AAS03844/c
ID AAS03844 standard; DNA; 69 BP.
XX
XX AAS03844;
XX
XX 07-SEP-2001 (first entry)
XX
XX Synthetic gene shMOBP/E, PCR primer #4.
XX
XX shMOBP/E: PCR primer; ss; immunogenic epitope cluster; IEC;
KW synthetic human myelin-oligodendrocytic basic protein; autoantigen;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;
KW autoimmune hepatitis; thyroiditis; orchitis;
KW idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX W0200131037-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-IL00688.
XX
XX 27-OCT-1999; 99IL-0132611.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Ben-Nun A, Kerlero De Rosbo N, Sappler GP;
PI
XX WPI: 2001-300515/31.
XX
XX Novel synthetic human target autoantigen gene useful for treating
PT autoimmune diseases such as multiple sclerosis, insulin-dependent
PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis
PT

XX Example 2; Fig 9; 182bp; English.

PS The sequence represents a PCR primer used in the construction of
 CC a nucleic acid encoding shOBP/E (synthetic human myelin-oligodendrocytic
 CC basic protein containing immunogenic epitope clusters (IEC) from MOBP.
 CC The synthetic human target autoantigen genes of the invention comprise
 CC sequences coding for at least 2 IECs of autoantigen(s) related to a
 CC specific autoimmune disease. The synthetic human target autoantigen genes
 CC are useful for treating autoimmune diseases such as multiple sclerosis,
 CC insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia
 CC gravis, uveitis, autoimmune hepatitis, thyroiditis, insulinitis, orchitis,
 CC idiopathic thrombocytopenic purpura, and inflammatory diseases (Crohn's
 CC disease, ulcerative colitis). The synthetic human target autoantigen
 CC genes are also useful for diagnosis and/or monitoring the progression of
 CC the autoimmune disease.

XX Sequence 69 BP; 21 A; 21 C; 19 G; 8 T; 0 other;

Query Match 48.5%; Score 16; DB 22; Length 69;

Best Local Similarity 68.8%; Pred. No. 2.6e+03;

Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 acggggtacggagcggtcggtgagtcgacatcg 32

DB 64 ACTTGGCAGCGCGGTGCTGTCTTCG 33

RESULT 13

AA257423/C

ID AA257423 standard; DNA; 26 BP.

AC AA257423;

XX 07-APR-2000 (first entry)

DE Oligonucleotide PCR primer pair #3 primer #1.

XX PCR primer; Zaocys dhumnade; Tortoise plastron; Oviductus ranae;

KW discrimination; black snake; forest frog; oil; reagent box;

KW medicinal; ss.

XX Synthetic.

XX CN1232085-A.

XX 20-OCN-1999.

XX 31-MAR-1999; 99CN-0114133.

XX 31-MAR-1999; 99CN-0114133.

XX (UYNA-) UNIV NANJING.

XX Wang Y, Zhou K, Liu Z;

XX WPI; 2000-098492/09.

XX Polymerase chain reaction (PCR) determining primer for Zaocys dhumnade,
 PT Tortoise plastron and Oviductus ranae -

XX Claim 1; Page 1; 4pp; Chinese.

XX The present invention describes a special DNA sequence which can be used
 CC to synthesise three pairs of high-specificity primers useful for
 CC discriminating if black snake, tortoise plastron and forest frog oil
 CC are true or false by simple polymerase chain reaction (PCR) of their DNA.
 CC AA257419 to AA257424 represent specifically claimed primers from the
 CC present invention. The primers can be used to make a reagent box for
 CC discriminating medicinal materials with high speed and quality.

XX Sequence 26 BP; 6 A; 12 C; 1 G; 7 T; 0 other;

Query Match 47.3%; Score 15.6; DB 21; Length 26;

Best Local Similarity 81.8%; Pred. No. 3.5e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 gagcgtgtagtcgacatcg 32

DB 22 GAGCATGCTTGATGATCGG 1

RESULT 14

AA130308

ID AA130308 standard; DNA; 51 BP.

AC AA130308;

XX 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #3516.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;

KW amyloid protein; angiotensin; apoptosis related protein; cadherin;

KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KW complement related protein; cytochrome; kinesin; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;

KW multifactorial disease; autoimmune disease; infection;

KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

XX Claim 1; Page 2394; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX Sequence 51 BP; 13 A; 10 C; 19 G; 9 T; 0 other;

Mon Jul 1 08:40:55 2002

us-09-709-170a-4.szlm75.rng

1
2
3
4

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:40 ; Search time 334.55 Seconds
(without alignments)
24.229 Million cell updates/sec

Title: US-09-709-170A-4
Perfect score: 33
Sequence: 1 acggggtacggagcgtggtggtcgtcgtgt 33

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	33	100.0	33 1 US-08-217-082A-4	Sequence 4, Appl
2	33	100.0	33 2 US-08-465-485A-4	Sequence 4, Appl
3	33	100.0	33 3 US-09-080-285-4	Sequence 4, Appl
4	20	60.6	20 1 US-08-217-082A-3	Sequence 3, Appl
5	20	60.6	20 2 US-08-465-485A-3	Sequence 3, Appl
6	20	60.6	20 3 US-09-080-285-3	Sequence 3, Appl
7	17.6	53.3	40 4 US-09-018-138-16	Sequence 16, Appl
8	17.6	53.3	40 4 US-08-890-929-4	Sequence 4, Appl
9	16.2	49.1	59 1 US-08-508-448C-4	Sequence 4, Appl
10	15.4	46.7	36 1 US-08-411-795B-200	Sequence 200, App
11	15.4	46.7	36 1 US-08-463-319A-200	Sequence 200, App
12	15	45.5	57 2 US-08-484-905-7	Sequence 7, Appl
13	15	45.5	57 3 US-08-481-985B-7	Sequence 7, Appl
14	15	45.5	57 3 US-08-370-476-7	Sequence 7, Appl
15	14.8	44.8	35 4 US-09-264-693-6	Sequence 6, Appl
16	14.8	44.8	48 5 PCT-US95-11985A-30	Sequence 30, Appl
17	14.8	44.8	48 5 PCT-US95-11985A-31	Sequence 31, Appl
18	14.8	44.8	31 3 US-08-648-322-13	Sequence 13, Appl
19	14.6	44.2	45 1 US-08-294-770A-6	Sequence 6, Appl
20	14.6	44.2	45 2 US-08-448-735C-6	Sequence 6, Appl
21	14.6	44.2	62 4 US-08-994-962-9	Sequence 9, Appl
22	14.6	44.2	72 2 US-08-169-948B-17	Sequence 17, Appl
23	14.6	44.2	72 2 US-08-448-873-17	Sequence 17, Appl
24	14.6	44.2	72 2 US-08-382-452D-17	Sequence 17, Appl
25	14.4	43.6	36 2 US-08-750-128-10	Sequence 10, Appl
26	14.4	43.6	38 2 US-08-455-968E-48	Sequence 48, Appl
27	14.4	43.6	48 1 US-07-609-716-37	Sequence 37, Appl

C	28	14.4	43.6	48 1	US-07-609-716-38	Sequence 38, Appl
C	29	14.4	43.6	48 3	US-08-475-411A-37	Sequence 37, Appl
C	30	14.4	43.6	48 3	US-08-475-411A-38	Sequence 38, Appl
C	31	14.4	43.6	48 4	US-08-478-029A-37	Sequence 37, Appl
C	32	14.4	43.6	48 4	US-08-478-029A-38	Sequence 38, Appl
C	33	14.4	43.6	49 5	PCT-US94-05085A-27	Sequence 27, Appl
C	34	14.4	43.6	49 5	PCT-US94-05085-27	Sequence 27, Appl
C	35	14.4	43.6	56 1	US-08-344-820-3	Sequence 3, Appl
C	36	14.4	43.6	66 3	US-08-478-097A-34	Sequence 34, Appl
	37	14	42.4	24 5	PCT-US95-11985A-22	Sequence 22, Appl
	38	14	42.4	24 5	PCT-US95-11985A-25	Sequence 25, Appl
	39	14	42.4	24 5	PCT-US95-11985A-35	Sequence 35, Appl
	40	14	42.4	36 4	US-09-041-878-2	Sequence 2, Appl
	41	14	42.4	39 3	US-09-042-105-27	Sequence 18, Appl
	42	14	42.4	60 5	PCT-US95-11985A-18	Sequence 81, Appl
	43	14	42.4	69 2	US-08-790-963-81	Sequence 81, Appl
	44	14	42.4	69 4	US-09-371-77A-81	Sequence 81, Appl
C	45	13.8	41.8	26 3	US-08-646-538-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-217-082A-4
; Sequence 4, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/286,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
US-08-217-082A-4

Query Match 100.0%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGGTACGAGGCTGGTAGTGCATCTGGT 33

RESULT 2

US-08-465-485A-4
; Sequence 4, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-4

Query Match 100.0%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGGTACGAGGCTGGTAGTGCATCTGGT 33

RESULT 3
US-09-080-285-4
; Sequence 4, Application US/09080285

; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-4

Query Match 100.0%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGGTACGAGGCTGGTAGTGCATCTGGT 33

RESULT 4

US-08-217-082A-3/C
; Sequence 3, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/217,082A
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-3

Query Match 60.6%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtagtgatc 29
|||||
DB 20 GGAGCTGGTAGTGATC 1

RESULT 5
US-08-465-485A-3/C
Sequence 3, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-3

Query Match 60.6%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtagtgatc 29
|||||
DB 20 GGAGCTGGTAGTGATC 1

RESULT 6
US-09-080-285-3/C
Sequence 3, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-3

Query Match
Best local Similarity 60.6%; Score 20; DB 3; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtagtgcac 29
|||||
DB 20 GGAGGCTGGTAGTGCAFC 1

RESULT 7
US-09-018-138-16/c
Sequence 16, Application US/09018138
Patent No. 6187564
GENERAL INFORMATION:
APPLICANT: Sytkowski, Arthur J.
TITLE OF INVENTION: Production and Use of Recombinant
FILE REFERENCE: BtH97-05A
CURRENT APPLICATION NUMBER: US/09/018,138
EARLIER FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 40
TYPE: DNA
ORGANISM: Human
US-09-018-138-16

Query Match
Best local Similarity 53.3%; Score 17.6; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 acgggtagcggagctggtagtgcac 32
|||||
DB 32 ACAGGGACAGAGCCGGGGTGTGATCTGC 1

RESULT 8
US-08-890-929-4/c
Sequence 4, Application US/08890929A
Patent No. 6242570
GENERAL INFORMATION:
APPLICANT: Sytkowski, Arthur J.
TITLE OF INVENTION: PRODUCTION AND USE OF RECOMBINANT
FILE REFERENCE: BtH97-05
CURRENT APPLICATION NUMBER: US/08/890,929A
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 40

TYPE: DNA
ORGANISM: Synthetic
US-08-890-929-4

Query Match
Best local Similarity 53.3%; Score 17.6; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 acgggtagcggagctggtagtgcac 32
|||||
DB 32 ACAGGGACAGAGCCGGGGTGTGATCTGC 1

RESULT 9
US-08-508-448C-4
Sequence 4, Application US/08508448C
Patent No. 5804410
GENERAL INFORMATION:
APPLICANT: Kazuyoshi YAMAKA et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,448C
FILING DATE: July 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: trachea
US-08-508-448C-4

Query Match
Best local Similarity 49.1%; Score 16.2; DB 1; Length 59;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gggtagcggagctggtagtgcac 23
|||||
DB 8 GGGCAGCAGAGCTGAGAGAG 28

RESULT 10

```

APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Multiple Mutation
TITLE OR INVENTION: Polypeptides
NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,319A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C2713/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-469-319A-200

Query Match          46.7%; Score 15.4; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 9, 2e+02;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY      1  accgggtacgagagcgtggtagatgtcatctggt 33
        | | | | | | | | | | | | | | | | | |
        2  AGGTTGTTCCGGGCTCCAGGAAAGCGACGGTGT 34

RESULT 12
US-08-484-905-7
; Sequence 7, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-905-7

Query Match 45.5%; Score 15; DB 2; Length 57;
Best Local Similarity 67.7%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3 ggggtagcagagcctgggtaggtgcatctggt 33
DB 9 ggggtagcagatccgagcggtggtcggtcggt 39

RESULT 13
US-08-481-985B-7
Sequence 7, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-985B-7

Query Match 45.5%; Score 15; DB 3; Length 57;
Best Local Similarity 67.7%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3 ggggtagcagagcctgggtaggtgcatctggt 33
DB 9 ggggtagcagatccgagcggtggtcggtcggt 39

RESULT 14
US-08-370-476-7
Sequence 7, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-370-476-7

Query Match 45.5%; Score 15; DB 3; Length 57;
Best Local Similarity 67.7%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 3 ggggtacggaggctggtagtcacatctgt 33
||||| ||||| | | ||||| |||||
Db 9 GGGGATCGGATCCGCGAGCGCGTGATCCGCT 39

RESULT 15
US-09-264-693-6/c
Sequence 6, Application US/09264693
Patent No. 6261760
GENERAL INFORMATION:
APPLICANT: Fielding, Christopher E
APPLICANT: Fielding, Phoebe E
TITLE OF INVENTION: REGULATION OF THE CELL CYCLE BY STEROLS
FILE REFERENCE: 2500.141US1 Regulation of cell cycle
CURRENT APPLICATION NUMBER: US/09/264,693
EARLIER FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 60/077,351
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Probe cav-646
US-09-264-693-6

Query Match 44.8%; Score 14.8; DB 4; Length 35;
Best Local Similarity 73.1%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 8 acggaggctggtagtcacatctgt 33
||||| ||||| | | ||||| |||||
Db 35 AAGGATCTGTGTGGTGCCTGTGCT 10

Search completed: June 28, 2002, 22:16:41
Job time: 8267 sec

1
2
3
4

	Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	acaaagcatcctgcagt	20							
Db	1	ACAAAGCATCTCTGCAGTTG	20							

RESULT	2			
LOCUS	196086	20 bp	DNA	PAT 01-DEC-1998
DEFINITION	Sequence 5 from patent US 5734033.			
ACCESSION	196086			
VERSION	196086.1	GI:3940556		
KEYWORDS	.			

REFERENCE	1 (bases 1 to 20)	
AUTHORS	Reed, J.	
TITLE	Antisense oligonucleotides inhibiting human bcl-2 gene expression	
JOURNAL	Patent: US 5734033-A 5 31-MAR-1998;	
FEATURES	Location/Qualifiers	
source	1..20	
	/organism="unknown"	
BASE COUNT	6 a 5 c 5 g	4 t
ORIGIN		

Query Match	100.0%	Score	20	DB	6	Length	20
Best Local Similarity	100.0%	Pred. No.	5.7				
Matches	20	Conservative	0			Indels	0
						Gaps	0

```
QY 1 acaagcgcctcctgcagttg 20
    |||||
Db 1 ACAAGGCATCCTGCAGTTG 20
```

RESULT	3			
AR052608/c				
LOCUS	AR052608	36 bp	DNA	linear
DEFINITION	Sequence	6 from patent	US 5831066.	
ACCESSION	AR052608			
VERSION	AR052608.1	GI:5975972		
KEYWORDS				

REFERENCE	1.....(bases 1 to 36)		
AUTHORS	Reed,J.C.		
TITLE	Regulation of bcl-2 gene expression		
JOURNAL	Patent: US 5831066-A 6 03-NOV-1998;		
FEATURES	Location/Qualifiers		
source	1..36		
	/organism="unknown"		
BASE COUNT	7 a	11 c	10 g
ORIGIN			8 t

Query Match	100.0%	Score 20;	DB 6;	Length 36;
Best Local Similarity	100.0%;	Prod. No. 5.6;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
0Y	1	acaaagcatctcgtcagttg	20	
DB	24	ACAAAGCATCTCTGCAGTTG	5	

RESULT	4			
196087/c				
LOCUS	196087	36 bp	DNA	linear
DEFINITION	Sequence 6 from patent US 5734033.			
ACCESSION	196087			
VERSION	196087.1	GI:3940557		

KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
Unknown.	Unknown.	Unclassified.	1 (bases 1 to 36)	Read, J.	Artisense oligonucleotides inhibiting human bcl-2 gene expression	Patent: US 5734033-A 6 31-MAR-1998.	Location/Qualifiers	7 a 11 c 10 g 8 t	
							1..36	/organism="unknown"	

Query Match	100.0%	Score 20	DB 6	Length 36
Best Local Similarity	100.0%	Pred. No.	5 6	
Matches 20	Conservative 0	Mismatches	0	Gaps 0

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QY      1  acaaagcattcctgcagttg  20
          |||||
Db      24  ACAAGGCATCCTGCAGTTG  5
```

RESULT	5			
AR109663/c				
LOCUS	AR109663	27 bp	DNA	1 linear
DEFINITION	Sequence 87 from patent US 6114139.			
ACCESSION	AR109663			
VERSION	AR109663.1	GI:12825939		

REFERENCE	1 (bases 1 to 27)
AUTHORS	Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukushima,S. and Ohgi,K.
TITLE	G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL	Patent: US 6114139-A 87-05-SEP-2000;
FEATURES	Location/Qualifiers
source	/..27
	/organism="unknown"
BASE COUNT	3 a 7 c 5 g 12 t
ORIGIN	

Query Match	76.0%	Score 15.2;	DB 6;	Length 27;
Best Local Similarity	85.0%	Pred. No. 2.7e+03;		
Matches 17, Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```

QY      1 acaaaagcattcctgcagttg 20
          | | | | | | | | | | | |
Db      25 AGAAGGCATCCAGCAGATG 6

```

RESULT	6			
LOCUS	ARI09666/c			
DEFINITION	Sequence	27 bp	DNA	linear
ACCESSION	ARI09666	90	from patent	US 6114139.
VERSION	ARI09666.1		GI:12825942	
KEYWORDS	.			
				PAT 14-FEB-2001

```

REFERENCE      Unclassified.
                1 (bases 1 to 27)
AUTHORS        Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE          G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL        Patent: US 6114139-A 90 05-SEP-2000;
FEATURES       Location/Qualifiers
                1..27
                /organism="unknown"
BASE COUNT     2 a      7 c      6 g      12 t
ORIGIN

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REFERENCE 1 (bases 1 to 30)
AUTHORS Nelson, P.S., Hood, L., and Lin, B.
TITLE Prostate-specific polynucleotides, polypeptides and their methods of use
JOURNAL Patent: WO 0065067-A, 26 02-NOV-2000;
The University of Washington (US)
FEATURES
source
1. .30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PRC Primer"
misc_binding
1. .30
/bound_moiety="TMPS22 gene specific primer U75329-71R"
BASE COUNT 8 a 7 c 5 g 10 t
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 caaagcactcgcagctt 19
||||| ||||| ||| |||
Db 7 CAAAGCCATCTTGCTGTT 24

RESULT 12
S60091 70 bp mRNA linear PRI 23-JUL-1993
LOCUS dystrophin (exon 43 directly spliced to exon 45) [human,
DEFINITION lymphocytes, mRNA Partial Mutant, 70 nt].
ACCESSION S60091
VERSION S60091.1 GI:300170
KEYWORDS
SOURCE human lymphocytes.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 70)
Narita, N., Nishio, H., Kitoh, Y., Ishikawa, Y., Ishikawa, Y.,
Minami, R., Nakamura, H. and Matsuo, M.
Insertion of a 5' truncated element into the 3' end of exon 44
of the dystrophin gene resulted in skipping of the exon during
splicing in a case of Duchenne muscular dystrophy
J. Clin. Invest. 91 (5), 1862-1867 (1993)
JOURNAL 93253023
MEDLINE
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI g1bbsg 131496] from the original journal article.
FEATURES
source
1. .70
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .70
/partial
/partial
/gene="dystrophin"
3. .62
/partial
/gene="dystrophin"
/gene="dystrophin"
/codon_start=1
/protein_id="AAD13910.1"
/db_xref="GI:4261610"
/translation="DRGNSRNALSGSKLSRH"
BASE COUNT 22 a 15 c 21 g 12 t
ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 70;
Best Local Similarity 83.3%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 caaagcactcgcagctt 19
||||| ||||| |||||
Db 32 CAATGCATCTTGAGACTT 15

RESULT 13
E36783
LOCUS Novel phoH. 21 bp DNA linear PAT 07-FEB-2001
DEFINITION E36783
ACCESSION E36783
VERSION E36783.1 GI:13022751
KEYWORDS JP 199253175-A/3.
SOURCE JP 199253175-A/3.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Magudarena, S.J.R.R.
TITLE Novel phoH
JOURNAL Patent: JP 199253175-A 3 21-SEP-1999;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 199253175-A/3
PD 21-SEP-1999
PF 18-SEP-1998 JP 1998303154
PR 18-SEP-1997 US 08/932978
PI MAGUDARENA SARA KAIN, JAMES RAYMOND BURADUN
PC C12N15/09, A61K31/00, A61K38/00, A61K39/395, C12P21/02, C12Q1/68,
PC GO1N33/15,
PC GO1N33/50, GO1N33/56, GO1N33/68, C12N15/09,
C12R1/46) PC C12N15/00,
PC A61K37/02, C12N15/00, C12R1/46)
CC Strandedness: Single;
CC Topology: linear;
FH Key
FT source
1. .21
Location/Qualifiers
1. .21
/organism="unidentified".
FEATURES
source
1. .21
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 8 a 6 c 4 g 3 t
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acaagcactcgcag 16
||||| ||||| |||
Db 1 ACAAGCCATCTTGCA 16

RESULT 14
E12037/c standard; DNA; UNC; 21 BP.
ID E12037
XX E12037;
XX E12037;
XX E12037;
SV E12037.1
SV
XX
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
DE PCR primer for detecting human tyrosine phosphatase, PTP-U2.
XX
XX
XX
XX
KW JP 1996242852-A/5.
OS unidentified
OC unclassified.
XX
XX
RN 1-21
RP
RA Tsuruo T., Kiyomiyu H.,
RT "TYROSINE DEPHOSPHORYLATION ENZYME AND GENE CODING FOR THE ENZYME";
Patent number JP1996242852-A/5, 24-SEP-1996.

RL MITSUBISHI CHEM CORP.

XX OS None
CC OC Artificial sequences.
CC PN JP 1996242852-A/5
CC PD 24-SEP-1996
CC PF 10-MAR-1995 JP 1995051374
CC PI TSURUO TAKASHI, KIYOMIYA HIROKUNI
CC PC C12N9/12,C12N1/21,C12N15/09,(C12N9/12,C12R1:19),(C12N9/12,
CC PC C12R1:91),
CC PC (C12N1/21,C12R1:19);
CC CC strandedness: Single;
CC CC topology: linear;
CC CC hypothetical: No;
CC CC anti-sense: Yes;
CC CC key Location/Qualifiers
CC FT source 1..21
CC FT /organism="Artificial sequences"
XX FT
FH key Location/Qualifiers
FH FT source 1..21
FT /db_xref="taxon:32644"
FT /organism="unidentified"
XX SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 other;

Query Match

Best Local Similarity 64.0%; Score 12.8; DB 23; Length 21;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 aagcatcctcagtt 19
||| |||||
Db 17 AAGTATCCTCGCAGTT 2

RESULT 15

ARI09662/c ARI09662 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6114139.
ACCESSION ARI09662
VERSION ARI09662.1 GI:12825938
KEYWORDS
SOURCE Unknown.

ORGANISM

Unknown.

Unclassified.

1 (bases 1 to 27)

REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 86 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27

BASE COUNT 0 a 8 c 7 g 12 t
ORIGIN /organism="unknown"

Query Match

Best Local Similarity 64.0%; Score 12.8; DB 6; Length 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acaagcatcctcga 16
|||||
Db 25 ACAAGCAGCAGCA 10

Search completed: June 28, 2002, 22:10:56
Job time: 8347 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:06 ; Search time 1381.16 Seconds
(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170a-5

Perfect score: 20

Sequence: 1 acaagacatcctgcagttg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_032802:*

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13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

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22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	19	AAV19655
2	20	100.0	36	16	AAQ86648
3	20	100.0	36	19	AAV19656
4	14.8	74.0	40	21	AAQ63894
5	14.8	74.0	51	22	AAI32869
6	14.2	71.0	30	21	AAQ9234
7	14.2	71.0	41	21	AAZ36900
8	13.6	68.0	45	19	AAV36324
9	13.6	68.0	57	14	AAQ34907

10	13.6	68.0	57	18	AAV77691
11	13.4	67.0	20	20	AAV69904
12	13.4	67.0	21	20	AAQ26507
13	13.2	66.0	20	21	AAQ00976
14	13.2	66.0	30	21	AAQ83346
15	13	65.0	43	16	AAQ02537
16	13	65.0	50	22	AAI29366
17	12.8	64.0	21	17	AAQ48483
18	12.8	64.0	21	20	AAI19906
19	12.8	64.0	23	20	AAQ25698
20	12.8	64.0	25	22	AAQ26064
21	12.8	64.0	30	16	AAQ93139
22	12.8	64.0	31	22	AAI31007
23	12.8	64.0	39	22	AAH91394
24	12.8	64.0	74	18	AAV77660
25	12.6	63.0	21	19	AAV24200
26	12.6	63.0	24	22	AAQ44587
27	12.6	63.0	24	24	AB191326
28	12.6	63.0	24	24	AB191327
29	12.6	63.0	28	13	AAQ22070
30	12.6	63.0	28	13	AAQ24348
31	12.6	63.0	29	20	AAQ81807
32	12.6	63.0	30	18	AAQ43800
33	12.6	63.0	31	22	AAQ07160
34	12.6	63.0	31	22	AAQ74954
35	12.6	63.0	33	16	AAQ87501
36	12.6	63.0	43	22	AAQ90375
37	12.6	63.0	45	11	AAQ06062
38	12.6	63.0	46	22	AAH75621
39	12.6	63.0	57	22	AAQ81686
40	12.6	63.0	60	19	AAV13217
41	12.6	63.0	70	21	AAQ98079
42	12.6	63.0	71	21	AAQ25875
43	12.4	62.0	22	24	AAQ97492
44	12.4	62.0	31	22	AAQ83560
45	12.4	62.0	33	14	AAQ45900

ALIGNMENTS

RESULT 1	
AAV19655	
ID AAV19655 standard; DNA: 20 BP.	
XX	
AC AAV19655;	
XX	
DT 12-JUN-1998 (first entry)	
XX	
DE Human bcl-2 antisense oligonucleotide 3.	
XX	
KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;	
KW cancer; ss.	
XX	
OS Synthetic.	
OS Homo sapiens.	
XX	
PN US5734033-A.	
XX	
PD 31-MAR-1998.	
XX	
PF 24-MAR-1994;	94US-0288692.
XX	
PR 21-FEB-1992;	92US-0840716.
PR 22-DEC-1988;	88US-0288692.
PR 24-MAR-1994;	94US-0217082.
XX	
PA (UYPE-) UNIV PENNSYLVANIA.	
XX	
PI Read J;	
XX	
DR WPI; 1998-229881/20.	

Staphylococcus aur
PCR primer used to
898001 PCR primer
Primer #2 for TOPP
Primer 075329-71R.
Vaccinia virus ORF
Human SNP oligonuc
Human tyrosine dep
Streptococcus pneu
Oligonucleotide M1
Human pT-1 gene e
Pig BDNF cDNA prob
Human single nucle
Human inflammatory
Staphylococcus aur
Homo sapiens BARD1
Mouse DBS-induced
Capture oligonucle
Sequence of forward
Oligonucleotide pri
Probe used to scre
Human IAP gene pr
Bacteriophage lamb
Bacteriophage lamb
MCP-N5 PCR primer.
pCAF: MERT1 PCR pr
Probe used to isol
OmpC His-tag fusio
HIV protease detec
Primer AS6 for mou
B. subtilis luma
Synthetic RNA olig
Murine SMC1 gene-s
Human dystrophin 9
HTLV-1 capture pro

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX
 PS Claim 6; Columns 3-4; 21pp; English.

CC This antisense oligonucleotide is complementary to the splice acceptor
 CC site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are
 CC phosphorothioate derivatives and can straddle strategic sites such as the
 CC translation initiation site, donor and acceptor splicing sites, or sites
 CC for transportation or degradation. Blocking translation at such strategic
 CC sites prevents the formation of a functional bcl-2 gene product. These
 CC oligonucleotides may be used for treating cancers associated with high
 CC levels of bcl-2 gene expression, especially lymphomas and some
 CC leukaemias.

SO Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgcagttg 20

Db 1 acaagcctcctgcagttg 20

RESULT 2

AA086648/C

ID AA086648 standard; DNA; 36 BP.

XX

AA086648;

XX 27-SEP-1995 (first entry)

DE Bcl-2 splice acceptor site.

XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;

XX ss.

OS Synthetic.

PN WO9508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US10725.

XX 20-SEP-1993; 93US-0124256.

XX (REED/) REED J C.

PI Reed JC;

XX WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumors, esp. breast cancer

PS Disclosure; Page 13; 108pp; English.

CC The antisense oligonucleotide SA-AS (AA086647) is complementary to a
 CC portion of the splice acceptor site of the pre-mRNA coding strand of
 CC the human bcl-2 gene. It reduces the expression of bcl-2 gene product,
 CC thereby inducing programmed cell death of certain cancer cells. The
 CC corresp. bcl-2 sense splice acceptor site region was synthesized for
 CC use as a control.

SO Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgcagttg 20

Db 24 ACAAGGCATCTGCACTTG 5

RESULT 3

AAV19656/C

ID AAV19656 standard; DNA; 36 BP.

XX AAV19656;

DE 12-JUN-1998 (first entry)

XX Human bcl-2 oligonucleotide 3.

XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

PN US5734033-A.

XX 31-MAR-1998.

XX 24-MAR-1994; 94US-0288692.

XX 21-FEB-1992; 92US-0840716.

XX 22-DEC-1988; 88US-0288692.

XX 24-MAR-1994; 94US-0217082.

XX (TYPE-) UNIV PENNSYLVANIA.

XX Reed J;

XX WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Disclosure; Columns 3-4; 21pp; English.

CC This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the splice acceptor site of the human
 CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.

SO Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgcagttg 20

Db 24 ACAAGGCATCTGCACTTG 5

RESULT 4

AAC63894/C

ID AAC63894 standard; DNA; 40 BP.

XX AAC63894;

PN WO200020445-A2.
 XX 13-APR-2000.
 PD
 XX
 PF 15-SEP-1999; 99WO-IB01664.
 XX
 PR 02-OCT-1998; 98US-0165863.
 PR 09-APR-1999; 99US-0289350.
 XX
 PA (CHAU)/ CHAU P.
 PA (LUTIT)/ LUTTEN R.
 PA (DEMO)/ DEMOTTE N.
 PA (DEFF)/ DEFOUR M.
 PA (LUSO)/ LUSQUIN C.
 PA (TRAV)/ TRAVERSARI C.
 PA (STRO)/ STROOBANT V.
 PA (CORN)/ CORNELIS G R.
 PA (BOON)/ BOON-FALLEUR T.
 PA (VBRU)/ VAN DER BRUGGEN P.
 XX
 PI Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
 PI Schults E, Warnier G;
 DR WPI: 2000-303739/26.
 XX
 XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
 PT stimulation and testing of lymphocytes with antigen presenting cells
 PT which present antigens derived from different expression systems
 XX
 XX Example 1; Page 38; 99pp; English.
 XX
 CC AAA09228-35 are primers to amplify MAGE cDNA. The MAGE cDNA was linked
 CC in-frame to a sequence encoding a truncated Yope (Yope 1-130). Vectors
 CC containing this sequence were used to generate recombinant Yersina.
 CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
 CC comprising successive steps of stimulation and testing of lymphocytes
 CC with antigen presenting cells (APCs) which present antigens derived
 CC from different expression systems. The CTL clones isolated recognize
 CC specific antigenic peptides of proteins, preferably of the MAGE family.
 CC The APC is autologous and each expression systems is different from at
 CC least one of the other expression systems, therefore isolating a
 CC cytotoxic T cell clone specific for the protein. The method can also be
 CC used to identify an antigenic peptide epitope. Isolated CTL clones
 CC are specific for a peptide/human leukocyte antigen (HLA) complex are
 CC claimed. The CTL cells specific for the complexes, peptides or cells
 CC which present the complexes on the cell surface are useful for treating
 CC pathological conditions characterized by abnormal expression of the
 CC complexes.
 CC
 CC Sequence 30 BP; 7 A; 9 C; 7 G; 7 T; 0 other;
 XX
 SO
 QY Query Match 71.0%; Score 14.2; DB 21; Length 30;
 DB Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 caaagcatcctgcagtg 20
 ||| ||||| ||| ||
 DB 3 cagagtcactctgcagtg 21
 ||| ||||| ||| ||
 RESULT 7
 ID AAV36900 standard; DNA; 41 BP.
 XX
 AC AAV36900;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE PCR primer used to amplify the yeast FUS1 promoter sequence.
 XX
 KW Activator of G protein signalling; AGS; ras-related G protein;

KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; FUS1 promoter; PCR primer; ss.
 XX
 OS Synthetic.
 OS Saccharomyces cerevisiae.
 XX
 PN WO9958670-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10151.
 XX
 PR 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Cismowski M, Duzic E;
 PI WPI: 2000-072337/06.
 DR
 XX
 PT A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Disclosure; Page 141; 162pp; English.
 XX
 CC PCR primers AAV36900-01 were used to amplify the yeast FUS1 promoter
 CC sequence. The amplified fragment was used to construct host yeast
 CC strains for use in a screening assay to identify a protein which
 CC is an activator of G protein signalling (AGS protein). The AGS
 CC cDNA sequence was isolated from a human liver cDNA library. The AGS
 CC protein exhibits homology to ras-related G proteins, and contains
 CC alterations in conserved amino acids consistent with a deficiency in
 CC GTP hydrolysis activity. AGS stimulates G protein activity, G
 CC protein-coupled signal transduction and the pheromone response pathway
 CC in a receptor-independent manner. The AGS protein also shows G-gamma
 CC selectivity, as measured by growth assays in yeast expressing various
 CC mammalian G-gamma constructs, and tissue-specific expression, as
 CC measured by Northern blot analysis. The AGS protein can be used to
 CC screen for compounds that modulate cellular signal transduction. The
 CC protein is used to treat disorders characterized by an aberrant
 CC AGS protein activity or AGS nucleic acid expression.
 CC
 CC Sequence 41 BP; 8 A; 11 C; 11 G; 11 T; 0 other;
 XX
 SO
 QY Query Match 71.0%; Score 14.2; DB 21; Length 41;
 DB Best Local Similarity 84.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 acaagcatcctgcagtg 19
 ||| ||||| ||||| ||
 DB 36 AAAAGGCATCTGCAGAT 18
 ||| ||||| ||||| ||
 RESULT 8
 ID AAV36324 standard; DNA; 45 BP.
 XX
 AC AAV36324;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human GABA receptor epsilon subunit DNA probe 1.
 XX
 KW GABA receptor; gamma-amino butyric acid receptor; human;
 KW appetite; cognition; probe; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9823742-A1.

XX 04-JUN-1998.
 XX 18-NOV-1997; 97WO-GB03159.
 XX 03-OCT-1997; 97GB-0020995.
 PR 25-NOV-1996; 96GB-0024442.
 XX (MERI) MERCK SHARP & DOHME LTD.
 XX Whiting PJ;
 PI WPI. 1998-322722/28.
 DR New isolated GABA receptor subunit, epsilon - used to develop
 PT products for the screening and design of drugs, e.g. for modulating
 PT appetite behaviours, hormonal interactions and cognition
 XX Example 3; Page 20; 37pp; English.
 PS Antisense oligonucleotide probes 1 and 2 (see AAV36325) are based
 CC on human GABA receptor novel epsilon subunit cDNA (see AAV36319).
 CC Each was radiolabelled at the 3' end with (35S)deoxyadenosine
 CC 5'-(thiotriphosphate) and used in in situ hybridisation assays
 CC to localise the epsilon subunit in monkey brain. The localisation
 CC appeared to be very restricted, residing mainly in the hypothalamus
 CC and arcuate nucleus. The new GABA receptor epsilon subunit (see
 CC AAV61045) can be used in the screening and design of drugs which act
 CC on the GABA receptor and which may be useful e.g. for the modulation
 CC of appetite behaviours, hormonal interactions and cognition.
 XX Sequence 45 BP; 9 A; 13 C; 11 G; 12 T; 0 other;

Query Match 68.0%; Score 13.6; DB 19; Length 45;
 Best local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 acaaggcatctgcagtgg 20
 ||||| ||||| |||||
 DB 29 ACMAAGCTTCGTGATGTTG 10

RESULT 9
 AAQ34907/c
 ID AAQ34907 standard; DNA; 57 BP.

AC AAQ34907;
 XX 10-MAY-1993 (first entry)
 DE PCR primer #63 used to make LHR chimaeras.
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;
 KM human chorionic gonadotropin; glycoprotein hormone receptor;
 KM chimaera: chimera.

XX Chimaeric; homo sapiens.
 OS

XX MO9222667-A.
 PD 23-DEC-1992.
 XX

PF 12-JUN-1992; 92WO-US04987.
 XX

PR 14-JUN-1991; 91US-0715911.
 XX

PA (UYNE-) UNIV NEW JERSEY.
 XX

PI Bernard M, Moyle WR, Myers R;
 XX

WPI; 1993-018150/02.
 DR

PT Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotropin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX Example 34; Page 37; 103pp; English.
 PS This PCR primer was used with AAQ34908 in the construction of a
 CC vector coding for an LH receptor analogue.
 CC
 XX Sequence 57 BP; 13 A; 10 C; 19 G; 15 T; 0 other;

Query Match 68.0%; Score 13.6; DB 14; Length 57;
 Best local Similarity 80.0%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 acaaggcatctgcagtgg 20
 ||||| ||||| |||||
 DB 48 ACACAGCATCAGACACTTG 29

RESULT 10
 AAV77691
 ID AAV77691 standard; DNA; 57 BP.

AC AAV77691;
 XX

DT 16-MAR-1999 (first entry)
 XX

DE Staphylococcus aureus contig SEQ ID #3380.
 XX

KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.

XX Staphylococcus aureus.
 OS

PN EP786519-A2.
 PD 30-JUL-1997.
 XX

PF 07-JAN-1997; 97EP-0100117.
 XX

PR 05-JAN-1996; 96US-0009861.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 PI Rosen CA;
 XX

DR WPI; 1997-374922/35.
 XX

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus
 PT stored on computer readable medium and used in the production of
 PT anti-S.aureus vaccines
 XX

PS Claim 1; Page 2535; 3271pp; English.
 XX

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the Invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.

SO Sequence 57 BP; 23 A; 8 C; 10 G; 16 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 57;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 acaagcattcctgacgttg 20
1 acaagcattcctgacgttg 20

RESULT 11

AAV69904/C
ID AAV69904 standard; DNA; 20 BP.

AC AAV69904;

DT 18-FEB-1999 (first entry)

DE PCR primer used to amplify heat-resistant maltose phosphorylase DNA.

KW Heat-resistant maltose phosphorylase; Bacillus RK-1; PCR primer; ss.

OS Synthetic.

XX Bacillus sp.

PN JP10262683-A.

PD 06-OCT-1998.

PF 25-MAR-1997; 97JP-0109996.

PR 25-MAR-1997; 97JP-0109996.

PA (SHOS) SHOWA SANGYO CO.

DR WPI; 1999-002482/01.

PT Nucleic acid encoding recombinant heat-resistant maltose
production of the enzyme

PS Example 1; Page 8; 27pp; Japanese.

CC PCR primers AAV69904-05 were used to amplify DNA encoding recombinant

CC heat-resistant maltose phosphorylase from Bacillus sp. RK-1 genomic

CC DNA. The enzyme reversibly phosphorylates maltose and has an optimum

CC temperature of 60-70 degrees Celsius for maltose phosphorylase.

SO Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 other;

OY 3 aagcattcctgacgttg 17
1 aagcattcctgacgttg 17

RESULT 12

AAV69904/C
ID AAV69904 standard; DNA; 21 BP.

AC AAV69904;

DT 21-SEP-2000 (first entry)

DE Primer #2 for TOP5 CAPS marker to map Arabidopsis thaliana PAD4 gene.

KW PAD4; disease resistance; phytoalexin; PR-1; PR-5;

KW pathogenesis-related protein; BGL2; beta-glucanase; ASA1;

KW anthranilate synthase; defence response; salicylic acid; SA;

KW signal transduction; transgenic plant; pathogen; bacteria; fungi;

KW nematode; Phytophthora; Peronospora; Pseudomonas; plant; agronomy;

KW crop; chromosome 3; pad4-1; PCR primer; TOP5 CAPS marker;

DT 26-MAR-2002 (first entry)

DE 898001 PCR primer used to generate alpha (1, 3) GT exon 9 DNA.

KW Xenotransplantation; Gal-alpha (1,3)Gal; GAL determinant; surgery;

KW alpha(1,3) galactosyltransferase; alpha (1, 3) GT; drug screening;

XX gene therapy; PCR primer; ss.

OS Unidentified.

XX WO20018096-A2.

PN 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15765.

PR 15-MAY-2000; 2000US-204148P.

PR 13-JUN-2000; 2000US-0593316.

PA (GERO-) GERON CORP.

PI Denning C, Clark J;

DR WPI; 2002-089848/12.

XX New ovine tissue devoid of antibody-detectable Gal-alpha(1,3)Gal

PT determinants, for xenotransplantation, and in the treatment of the

PT human body by surgery or therapy

PS Example 2; Page 25; 86pp; English.

XX The patent discloses immunologically compatible animal tissue, suitable

CC for xenotransplantation into human patients. The invention also relates

CC to an ovine tissue devoid of antibody-detectable Gal-alpha (1,3)Gal (GAL)

CC determinants which are made by alpha(1,3) galactosyltransferase (GT). The

CC ovine tissue is useful for treatment of human body by surgery or therapy

CC and in xenotransplantation, by transplanting the ovine tissue into a

CC mammal having circulating antibody against Gal alpha(1,3)GT determinants.

CC Polynucleotide constructs of the invention are useful for inactivating

CC an alpha1,3 GT gene in an ovine cell. Alpha (1,3) GT sequences are useful

CC for drug screening and for the production of GAL containing synthetic

CC oligosaccharides. Sequences of the invention are also useful in gene

CC therapy. The present DNA sequence is a PCR primer which is used for

CC generating phage G alpha (1, 3) GT exon 9 DNA.

SO Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;

OY 2 caagcattcctgca 16
1 caagcattcctgca 16

Db 15 CAAAGCATCTCTGGA 1

RESULT 13

AAV69904/C
ID AAV69904 standard; DNA; 20 BP.

AC AAV69904;

DT 21-SEP-2000 (first entry)

DE Primer #2 for TOP5 CAPS marker to map Arabidopsis thaliana PAD4 gene.

KW PAD4; disease resistance; phytoalexin; PR-1; PR-5;

KW pathogenesis-related protein; BGL2; beta-glucanase; ASA1;

KW anthranilate synthase; defence response; salicylic acid; SA;

KW signal transduction; transgenic plant; pathogen; bacteria; fungi;

KW nematode; Phytophthora; Peronospora; Pseudomonas; plant; agronomy;

KW crop; chromosome 3; pad4-1; PCR primer; TOP5 CAPS marker;

PT DNA - is only viable in presence of complementation, useful for
PT vaccines

PS Example 3; Page 21; 67pp; English.

XX The expression of foreign proteins for use as vaccines involves the
CC construction of a defective poxvirus, pref. vaccinia, in which the DNA
CC encoding the foreign protein is inserted into a deleted essential
CC region of the virus. The defective viruses are only viable by
CC complementation which is provided by an external source e.g. as a plasmid
CC such as PCR11 contg. the required gene.
CC The primers AA702537-8 were used to amplify the vaccinia A8L open
CC reading frame (ORF) for the construction of a helper cell line contg. the
CC plasmid pSV-A8L-EDH. This plasmid contains the A8L gene (which encodes
CC the larger (82 kD) subunit of the vaccinia virus early transcription
CC factor (VETF)) under control of the SV40 promoter. It expresses the A8L
CC gene product in transfected monkey kidney Vero cells and can complement
CC the defective vaccinia virus d-A8L-2G, in which the wild type A8L gene is
CC replaced, by homologous recombination, with a defective A8L gene contg. a
CC lacZ-gpt expression cassette. The primers amplify the A8L sequence as a
CC 2.1 kb prod. which was cloned into PCR11 to produce PCR-A8Lt. This
CC plasmid was subsequently used to construct pSV-A8L-EDH.
XX
SQ Sequence 43 BP; 16 A; 6 C; 10 G; 11 T; 0 other;

Query Match

65.0%; Score 13; DB 16; Length 43;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gcatcctgcagtt 19
|||||

DB 14 GCATCCTGCAGTT 2

Search completed: June 28, 2002, 22:40:08
Job time: 8084 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:41 ; Search time 334.55 Seconds
(without alignments)
14.684 Million cell updates/sec

Title: US-09-709-170A-5

Perfect score: 20

Sequence: 1 acaagacatctgtcagttg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1 US-08-217-082A-5	Sequence 5, Appl1
2	20	100.0	20	2 US-08-465-485A-5	Sequence 5, Appl1
3	20	100.0	20	3 US-09-080-285-5	Sequence 5, Appl1
4	20	100.0	36	1 US-08-217-082A-6	Sequence 6, Appl1
5	20	100.0	36	2 US-08-465-485A-6	Sequence 6, Appl1
6	20	100.0	36	3 US-09-080-285-6	Sequence 6, Appl1
7	15.2	76.0	27	3 US-08-513-974B-87	Sequence 87, Appl1
8	13.8	69.0	27	3 US-08-513-974B-90	Sequence 90, Appl1
9	13.4	67.0	27	3 US-08-513-974B-89	Sequence 89, Appl1
10	13.4	67.0	30	3 US-08-513-974B-137	Sequence 137, Appl1
11	12.8	64.0	21	2 US-08-932-878-4	Sequence 4, Appl1
12	12.8	64.0	27	3 US-08-513-974B-86	Sequence 86, Appl1
13	12.8	64.0	28	1 US-07-971-819A-138	Sequence 138, Appl1
14	12.6	63.0	28	1 US-07-977-434-26	Sequence 26, Appl1
15	12.6	63.0	28	1 US-08-475-231-30	Sequence 26, Appl1
16	12.6	63.0	28	1 US-08-458-819-26	Sequence 26, Appl1
17	12.6	63.0	28	5 PCT-US91-07035-26	Sequence 26, Appl1
18	12.6	63.0	28	5 PCT-US91-07035-26	Sequence 26, Appl1
19	12.6	63.0	29	4 US-09-199-290-20	Sequence 13, Appl1
20	12.6	63.0	30	4 US-08-446-935-13	Sequence 13, Appl1
21	12.6	63.0	31	4 US-08-852-001-15	Sequence 15, Appl1
22	12.6	63.0	33	1 US-08-310-416A-7	Sequence 7, Appl1
23	12.6	63.0	33	2 US-08-888-171-7	Sequence 7, Appl1
24	12.6	63.0	46	4 US-09-507-323B-4	Sequence 4, Appl1
25	12.6	63.0	60	1 US-08-424-788-15	Sequence 15, Appl1
26	12.4	62.0	29	2 US-08-560-098A-39	Sequence 39, Appl1
27	12.4	62.0	33	4 US-08-427-569-48	Sequence 48, Appl1

C 28	12.4	62.0	35	3	US-08-785-247-19	Sequence 19, Appl1
C 29	12.4	62.0	39	2	US-08-414-657D-40	Sequence 40, Appl1
C 30	12.4	62.0	40	1	US-07-854-596B-54	Sequence 54, Appl1
C 31	12.4	62.0	40	1	US-07-854-596B-55	Sequence 55, Appl1
C 32	12.4	62.0	43	2	US-08-560-098A-40	Sequence 40, Appl1
C 33	12.4	62.0	59	1	US-07-859-453E-5	Sequence 5, Appl1
C 34	12.4	62.0	59	1	US-07-859-453E-7	Sequence 7, Appl1
C 35	12.4	62.0	59	1	US-07-859-453E-9	Sequence 9, Appl1
C 36	12.4	62.0	59	1	US-07-859-453E-11	Sequence 11, Appl1
C 37	12.4	62.0	64	6	5422249-11	Patent No. 5422249
C 38	12.2	61.0	17	4	US-08-584-040-7778	Sequence 7778, Ap
C 39	12.2	61.0	27	1	US-08-348-891A-19	Sequence 19, Appl1
C 40	12.2	61.0	27	1	US-08-905-817-19	Sequence 19, Appl1
C 41	12.2	61.0	27	3	US-08-513-974B-2	Sequence 2, Appl1
C 42	12.2	61.0	27	3	US-08-513-974B-76	Sequence 76, Appl1
C 43	12.2	61.0	27	4	US-08-776-971-30	Sequence 30, Appl1
C 44	12.2	61.0	33	1	US-08-299-249A-15	Sequence 15, Appl1
C 45	12.2	61.0	33	3	US-08-894-173-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-08-217-082A-5
Sequence 5, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCE ADDRESSES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-5

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcgcagttg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACAAGCCTCCTGCAGTTG 20

RESULT 2

US-08-465-485A-5
; Sequence 5, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-5

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcgcagttg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACAAGCCTCCTGCAGTTG 20

RESULT 3
US-09-080-285-5

; Sequence 5, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-5

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcgcagttg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACAAGCCTCCTGCAGTTG 20

RESULT 4
US-08-217-082A-6/c
; Sequence 6, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

US-08-217-082A-6/c
; Sequence 6, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-6

Query Match 100.0%; Score 20; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaagcattcctgcagttg 20
|||||
Db 24 ACAAGCATTCTGCAGTTG 5

RESULT 5
US-08-465-485A-6/c
Sequence 6, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-6

Query Match 100.0%; Score 20; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaagcattcctgcagttg 20
|||||
Db 24 ACAAGCATTCTGCAGTTG 5

RESULT 6
US-09-080-285-6/c
Sequence 6, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-6

Query Match 100.0%; Score 20; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acaagcctcctgcagtgt 20
|||||
Db 24 ACAAGCCTCCTGCAGTGT 5

RESULT 7
US-08-513-974B-87/C
Sequence 87 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-87

Query Match 76.0%; Score 15.2; DB 3; Length 27;
Best Local Similarity 85.0%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acaagcctcctgcagtgt 20
|||||
Db 25 ACAAGCCTCCTGCAGTGT 6

RESULT 8
US-08-513-974B-90/C
Sequence 90 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: PCT/JP95/01599
3      FILING DATE: 10-AUG-1995
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: JP 7-093989
6      FILING DATE: 19-AUG-1995
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: JP 7-057186
9      FILING DATE: 16-MAR-1995
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: JP 7-007177
12     FILING DATE: 20-JAN-1995
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: JP 6-32611
15     FILING DATE: 28-DEC-1994
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: JP 6-270017
18     FILING DATE: 02-NOV-1994
19     PRIOR APPLICATION DATA:
20     APPLICATION NUMBER: JP 6-236357
21     FILING DATE: 30-SEP-1994
22     PRIOR APPLICATION DATA:
23     APPLICATION NUMBER: JP 6-236356
24     FILING DATE: 30-SEP-1994
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: JP 6-189274
27     FILING DATE: 11-AUG-1994
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: JP 6-189273
30     FILING DATE: 11-AUG-1945
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: JP 6-189272
33     FILING DATE: 11-AUG-1994
34     ATTORNEY/AGENT INFORMATION:
35     NAME: Resnick, David S.
36     REGISTRATION NUMBER: 34,235
37     REFERENCE/DOCKET NUMBER: 45753
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: 617-523-3400
40     TELEFAX: 617-523-6440
41     INFORMATION FOR SEQ ID NO: 90:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 27 base pairs
44     TYPE: nucleic acid
45     STRANDEDNESS: double
46     TOPOLOGY: linear
47     MOLECULE TYPE: CDNA
48     US-08-513-974B-90

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Query Match          69.0%;   Score 13.8;   DB 3;   Length 27;
Best Local Similarity 88.2%;   Pred. No.3.2e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

OY      1   acaagcgcatctgcag 17
        1   | | | | | | | | | |
Db      25   AGAAAGGCATCCAGCAG 9

RESULT 9
US-08-513-974B-89/C
; Sequence 89, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-169273
FILING DATE: 11-AUG-1945

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ. ID NO.: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-89

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RESULT 10
US-08-513-974B-137/C
Sequence 137, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtsuki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-137

Query Match 67.0%; Score 13.4; DB 3; Length 30;
Best Local Similarity 93.3%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 aaagcactcctgcag 17
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DB 23 AAAGCATCCTCAGCAG 9

RESULT 11
US-08-932-978-4
Sequence 4, Application US/08932978
Patent No. 5885804
GENERAL INFORMATION:
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
TITLE OF INVENTION: NOVEL PHO
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,978
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GH0100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-932-978-4

Query Match 64.0%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acaagcactcctgc 16
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DB 1 ACAAGCATCCTCAG 16

RESULT 12

US-08-513-974B-86/C
Sequence 86 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-86
Query Match 64.0%; Score 12.8; DB 3; Length 27;
Best local Similarity 87.5%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 25 ACAAGGACAGCAGCA 10
OY 1 acaaggacatcctgca 16
|||||
Db 25 ACAAGGACAGCAGCA 10
RESULT 13
US-08-513-974B-138/C
Sequence 138 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-138

Query Match 64.0%; Score 12.8; DB 3; Length 30;
Best local Similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acaaggcctctgca 16
DB 25 ACAAGGCACCCAGCA 10

RESULT 14
US-07-971-819A-30
Sequence 30, Application US/07971819A
Patent No. 5420029
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Scofield, Susanne C.
TITLE OF INVENTION: Purified Thermostable Nucleic Acid
TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,819A
FILING DATE: 19930203
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid

US-07-971-819A-30

Query Match 63.0%; Score 12.6; DB 1; Length 28;
Best local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

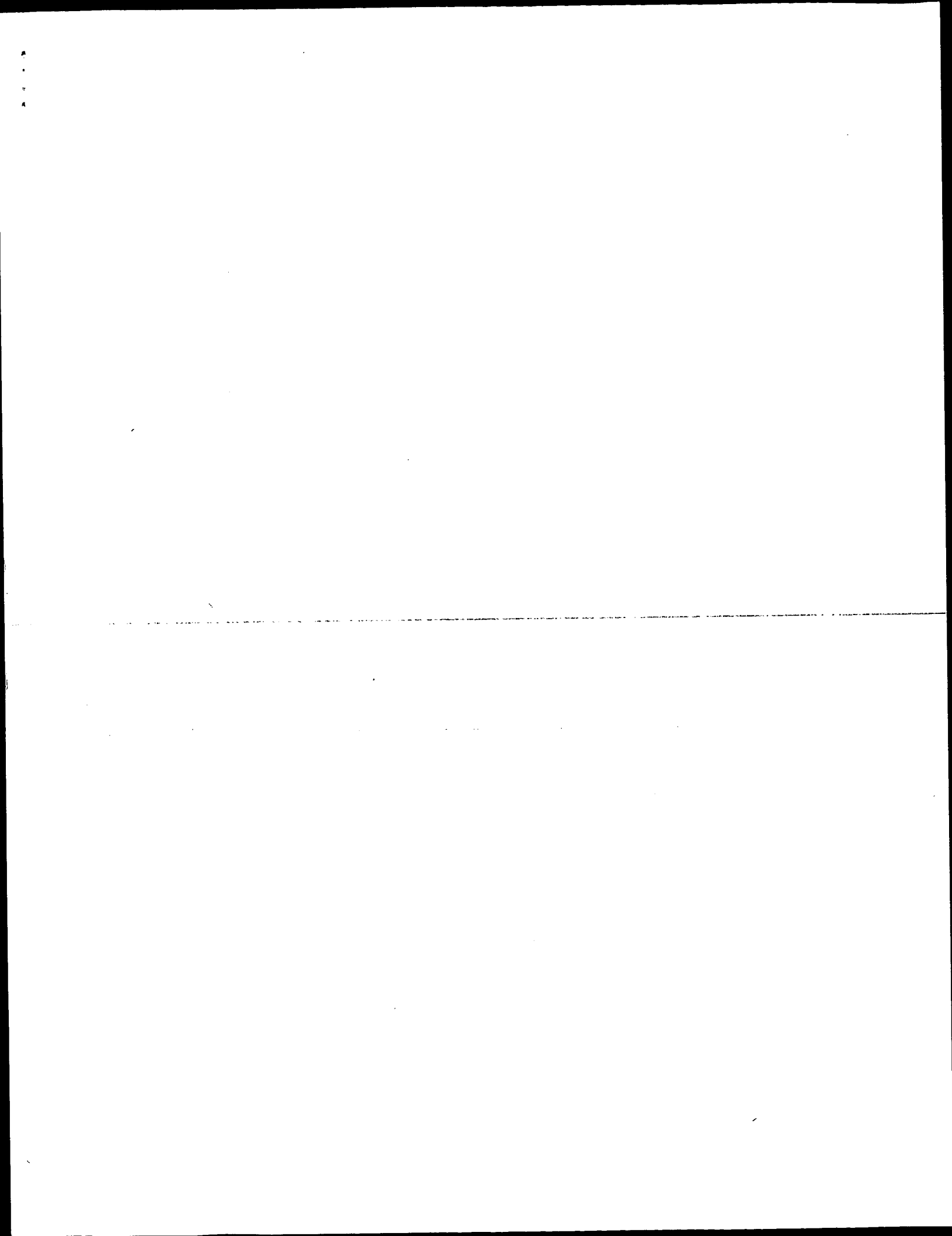
OY 1 acaaggcctctgcagt 19
DB 2 ATAAAGCAGCTTCAGCT 20

RESULT 15
US-07-977-434-26
Sequence 26, Application US/07977434
Patent No. 5466591
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 557,517
 FILING DATE: 24-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cseert
 REGISTRATION NUMBER: 31,922
 REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2972
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA primer FL63
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-07-977-434-26

Query Match 63.0%; Score 12.6; DB 1; Length 28;
 Best Local Similarity 78.9%; Pred No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 Db 2 ATAAGCATGCTTCAGCT 20

Search completed: June 28, 2002, 22:16:43
 Job time: 8269 sec



Mon Jul 1 08:40:57 2002

us-09-709-170a-6.szm75.rge

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:56 ; Search time 3762.88 Seconds
(without alignments)
200.207 Million cell updates/sec

Title: us-09-709-170a-6

Perfect score: 1 cccccacgcagatgccttcgtgaactgacg 36

Scoring table: IDENTITY-NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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33: em_hlg_inv: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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3	24	66.7	34	6	AR007302	AR007302 Sequence
4	20	55.6	20	6	AR052607	AR052607 Sequence
5	20	55.6	20	6	196086	196086 Sequence 5
6	16.8	46.7	51	6	AX163121	AX163121 Sequence
7	16.8	46.7	51	6	AX163122	AX163122 Sequence
8	16.8	46.7	60	5	ASXPTGR6	M38630 Aslyanax fa
9	15.8	43.9	42	9	S68042	S68042 hemoglobin
10	15.8	43.9	57	9	HSTCR4021	X58759 Human mRNA
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15	15.4	42.8	32	6	AR178019	AR178019 Sequence
16	15.4	42.8	35	6	AX08115	AX08115 Sequence
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19	15.2	42.2	20	6	AR121062	AR121062 Sequence
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26	15.2	42.2	40	6	AX180787	AX180787 Sequence
27	15.2	42.2	45	6	AR068214	AR068214 Sequence
28	15.2	42.2	60	6	AR076966	AR076966 Sequence
29	15.2	42.2	60	6	AR078799	AR078799 Sequence
30	15.2	42.2	60	6	AX136804	AX136804 Sequence
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36	15.2	42.2	60	9	AX127334	AX127334 Sequence
37	15.2	42.2	61	6	AR109475	AR109475 Sequence
38	15.2	42.2	63	6	AR109475	AR109475 Sequence
39	15.2	42.2	63	6	S60091	E16172 Hair pin-ly
40	15.2	42.2	70	9	AX249578	S60091 dystrophin
41	15.2	42.2	31	6	AX249578	AX249578 Sequence
42	15.2	42.2	49	6	AR164215	AR164215 Sequence
43	15.2	42.2	51	6	AX161217	AX161217 Sequence
44	15.2	42.2	51	6	AX161219	AX161219 Sequence
45	15.2	42.2	54	6	AR050475	AR050475 Sequence

ALIGNMENTS

RESULT 1	AR052608	36 bp	DNA	1 linear	PAT 29-SEP-1999
LOCUS	AR052608	6	from patent US 5831066.		
DEFINITION	Sequence				
ACCESSION	AR052608				
VERSION	AR052608.1	GI:5975972			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 36)				
AUTHORS	Reed,J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 6/03-NOV-1998;				
FEATURES	Location/Qualifiers				
SOURCE	1..36				
BASE COUNT	7 a 11 c 10 g 8 t				
ORIGIN					

Query Match 100.0%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccccaactgcagatgcttcttggaactgacg 36
Db 1 ccccaactgcagatgcttcttggaactgacg 36

RESULT 2
LOCUS 196087
DEFINITION Sequence 6 from patent US 5734033.
ACCESSION 196087
VERSION 196087.1 GI:3940557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Reed,J.
JOURNAL Antisense oligonucleotides inhibiting human bcl-2 gene expression
FEATURES
source Location/Qualifiers
1..36
BASE COUNT 7 a 11 c 10 g 8 t
ORIGIN

Query Match 100.0%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccccaactgcagatgcttcttggaactgacg 36
Db 1 ccccaactgcagatgcttcttggaactgacg 36

RESULT 3
LOCUS AR007302
DEFINITION Sequence 16 from patent US 5750390.
ACCESSION AR007302
VERSION AR007302.1 GI:3966786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 16 12-MAY-1998;
FEATURES
source Location/Qualifiers
1..34
BASE COUNT 6 a 9 c 11 g 8 t
ORIGIN

Query Match 66.7%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ggaatgccttggaactgacg 36
Db 1 ggaatgccttggaactgacg 24

RESULT 4
LOCUS AR052607
DEFINITION Sequence 5 from patent US 5831066.
ACCESSION AR052607

VERSION AR052607.1 GI:5975971
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
JOURNAL Regulation of bcl-2 gene expression
FEATURES
source Patent: US 5831066-A 5 03-NOV-1998;
1..20
BASE COUNT 6 a 5 c 5 g 4 t
ORIGIN

Query Match 55.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcagatgcttctgt 24
Db 20 CAACTGCAGATGCTTGT 1

RESULT 5
LOCUS 196086
DEFINITION Sequence 5 from patent US 5734033.
ACCESSION 196086
VERSION 196086.1 GI:3940556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.
JOURNAL Antisense oligonucleotides inhibiting human bcl-2 gene expression
FEATURES
source Patent: US 5734033-A 5 31-MAR-1998;
1..20
BASE COUNT 6 a 5 c 5 g 4 t
ORIGIN

Query Match 55.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcagatgcttctgt 24
Db 20 CAACTGCAGATGCTTGT 1

RESULT 6
LOCUS AX163121
DEFINITION Sequence 6449 from Patent WO0140521.
ACCESSION AX163121
VERSION AX163121.1 GI:14544452
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shinketsu,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
FEATURES
Patent: WO 0140521-A 6449 07-JUN-2001;
Curagen Corporation (US)
Location/Qualifiers

source 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (6450 is other entry)
Accession number c927837466"

BASE COUNT 10 a 18 c 12 g 11 t
ORIGIN

Query Match 46.7%; Score 16.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ccccaactgcagatgccttctggaactgacg 36
||| ||||| ||| ||||| ||| ||| |||
Db 10 CCACCACTGCTCGACCTTTGACGACCTGCTCGG 45

RESULT 7
AX163122 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX163122 6450 from Patent WO0140521.
DEFINITION Sequence
ACCESSION AX163122
VERSION AX163122.1 GI:14544453
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkens, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6450 07-JUN-2001;
Curation Corporation (US)
FEATURES
source 1. .51
Location/Qualifiers
misc_feature 26
/note="2 of 2 allelic variants (6449 is other entry)
Accession number c927837466"

BASE COUNT 10 a 19 c 12 g 10 t
ORIGIN

Query Match 46.7%; Score 16.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 1 ccccaactgcagatgccttctggaactgacg 36
||| ||||| ||| ||||| ||| ||| |||
Db 10 CCACCACTGCTCGACCTTTGACGACCTGCTCGG 45

RESULT 8
ASYPIGR6 60 bp DNA linear VRT 06-MAR-1995
LOCUS ASYPIGR6 60 bp DNA linear VRT 06-MAR-1995
DEFINITION Astyanax fasciatus red visual pigment gene (R007), exon 6.
ACCESSION M38630
VERSION M38630.1 GI:210992
KEYWORDS visual pigment.
SEGMENT 6 of 6
SOURCE Astyanax fasciatus DNA, clone lambda R007.
ORGANISM Astyanax mexicanus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Characiformes; Characidae; Tetraodonidae; Astyanax.

REFERENCE 1 (bases 1 to 60)
AUTHORS Yokoyama, R. and Yokoyama, S.
TITLE Convergent evolution of the red- and green-like visual pigment
genes in fish, Astyanax fasciatus, and human

JOURNAL PROC. Natl. Acad. Sci. U.S.A. 87 (23), 9315-9318 (1990)
MEDLINE 9106796
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by S. Yokoyama, 18-SEP-1990.
Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by S. Yokoyama, 18-SEP-1990.
Location/Qualifiers

FEATURES
source 1. .60
/organism="Astyanax mexicanus"
/db_xref="taxon:7994"
/clone="lambda-007"
join(M38625.1:1..103,M38626.1:11..307,M38627.1:11..179,
M38628.1:11..176,M38629.1:11..250,11..60)
/partial
/gene="R007"
/codon_start=1
/product="red visual pigment"
/protein_id="AA62672.1"
/db_xref="GI:210994"
/translation="MGDQMGDAVFAARRGGDPTREAFPTNTSNTKDPFEGPVYH
APRWVILATCMFEVYVASTYNGVLVASAFKRLRRLPILNVLNLAIALLETL
ASTISVNOFFGYFLIGHPMCVGEFTVATCGIAGLSLTVISMERNVYCKPQNVK
FDGRMAGIVYFWWSAVWCAPRIFGWSRYPHGLKTSQPDVSGSDPGVOSTMI
VLMTCCFPIPLGIIILCYIAVMMARIVVAGQODSDSTQKAERYSRMVVMIMAYCE
CMGPTPEFACFAANPGYAFHPPLAAMPVAFKSAATYVNVIVVFNNRFRVCIQOLF
GKRYDGS"

gene join(M38626.1:1..317,M38627.1:1..189,M38628.1:1..186,
M38629.1:1..260,1..60)
/gene="R007"
order(M38629.1:251..260,1..10)
/gene="R007"

INTRON /note="814 bp gap"

BASE COUNT 12 a 11 c 19 g 18 t
ORIGIN

Query Match 46.7%; Score 16.8; DB 5; Length 60;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 6 aactgcagatgccttctggaactgta 33
||| ||||| ||| ||||| ||| ||| |||
Db 33 AGCTGCATGATGCATACGCGGAACGTCA 6

RESULT 9
S68042 42 bp DNA linear PRI 07-MAY-1993
LOCUS S68042 42 bp DNA linear PRI 07-MAY-1993
DEFINITION hemoglobin beta chain [human, Genomic Mutant, 42 nt].
ACCESSION S68042
VERSION S68042.1 GI:239717
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 42)
AUTHORS Oner R., Oner, C., Wilson, J.B., Tamagnini, G.P., Ribeiro, L.M. and
Huisman, J.H.
TITLE Dominant beta-thalassemia trait in a Portuguese family is caused
by a deletion of (G)TGGTGGT(G) and an insertion of (G)GCGAG(G) in
codons 134, 135, 136 and 137 of the beta-globin gene
Br. J. Haematol. 79 (2), 306-310 (1991)
JOURNAL GenBank staff at the National Library of Medicine created this
entry [NCBI g1dbsg.68042] from the original journal article.
MEDLINE This sequence comes from Fig.2.
REMARK deletion of TG.GGT.GGT.GT at codons 134-137 (Val.Ala.Gly.Val) and
the insertion of GC.AG (Gly.Arg).
COMMENT Location/Qualifiers
FEATURES
source 1. .42

RESULT 11

BASE COUNT	5 a	11 c	7 g	8 t
ORIGIN				

RESULT 11

Mon Jul 1 08:40:57 2002

us-09-709-170a-6.szlm75.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:08 ; Search time 1381.16 Seconds
(without alignments)
44.751 Million cell updates/sec

Title:	US-09-709-170A-6
Perfect score:	36
Sequence:	1 cccccaactgcagatgccttctgtgaaactgtacgg 36

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 1996432
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Minimum DB seq length: 0
Maximum DB seq length: 75
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

Database :
N.GeneSeq_032802:*
1:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT.*
2:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT.*
3:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1982.DAT.*
4:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT.*
5:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1984.DAT.*
6:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1985.DAT.*
7:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1986.DAT.*
8:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1987.DAT.*
9:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1988.DAT.*
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11:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1990.DAT.*
12:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1991.DAT.*
13:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1992.DAT.*
14:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1993.DAT.*
15:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1994.DAT.*
16:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1995.DAT.*
17:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1996.DAT.*
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19:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1998.DAT.*
20:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1999.DAT.*
21:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2000.DAT.*
22:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT.*
23:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT.*
24:/SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT.*

```

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	36	100.0	36	16	AA086648	bcl-2 splice accept
2	36	100.0	36	19	AAV19656	human bcl-2 oligon
3	24	66.7	34	14	AA051962	bcl-2 mRNA ribozyme
c	20	55.6	20	19	AAV19655	Human bcl-2 antis
c	17.2	47.8	45	21	AAC65053	Human bcl genes
5	17	47.2	40	19	AAV36524	Human GABA recept
6	16.8	46.7	51	22	AAV79508	Human silent SNP c
7	16.8	46.7	51	22	AAV79509	Human silent SNP c
8	16.6	46.7	47	21	AAV28593	Human silent SNP c
9	16.6	46.1	47	21	AAV28593	PCR primer used fo

C	10	16.2	45.0	40	21	AA6C3894	Chinese hamster/FA
C	11	16	44.4	20	21	AAZ7381	PCR primer for hum
C	12	15.8	43.9	34	17	AA174539	Fc receptor PCR pr
C	13	15.8	43.9	36	10	AAAN0551	Tissue plasminogen
C	14	15.8	43.9	43	22	AAAC50375	pC4Fc:MEH1 PCR pr
C	15	15.6	43.3	31	24	AAAD24317	Human stat3 antise
C	16	15.6	43.3	41	21	AAAZ36900	PCR primer used to
C	17	15.4	42.8	31	22	AA131519	Human single nucle
C	18	15.4	42.8	51	22	AAH79972	Human DNA containi
C	19	15.2	42.2	20	21	AAAC3252	Mouse STAT3 phosph
C	20	15.2	42.2	20	21	AAAZ3647	Antisense oligonuc
C	21	15.2	42.2	20	22	AAAS1516	Human bcl-x antise
C	22	15.2	42.2	20	22	AAH27692	Human bcl-x antise
C	23	15.2	42.2	20	24	AAAS69849	Mouse STAT3 antise
C	24	15.2	42.2	23	22	AAAF24593	PCR primer used to
C	25	15.2	42.2	23	22	AAE24715	PCR primer used to
C	26	15.2	42.2	40	17	AAE69418	PCR primer used to
C	27	15.2	42.2	40	17	AAE69418	plasmid p1825fl c
C	28	15.2	42.2	43	22	AAAC90374	Circular plasmid e
C	29	15.2	42.2	43	22	AAAC90374	pFlag-CMV-5a:MEH1
C	30	15.2	42.2	51	22	AAAL33347	Human IL-17E hybri
C	31	15.2	42.2	51	22	AAAT29968	Human SNP oligonuc
C	32	15.2	42.2	60	17	AAAG94476	Fusion junction fo
C	33	15.2	42.2	60	21	AAAB89951	Vector pBR322 Scal
C	34	15.2	42.2	60	21	AAAB89952	pBR322 oligonucleo
C	35	15.2	42.2	60	22	AAAF24270	PCR322 oligonucleo
C	36	15.2	42.2	60	22	AAAF29102	ReclA ligation meth
C	37	15.2	42.2	60	22	AAAF29118	Oligonucleotide 1
C	38	15.2	42.2	61	22	AAAS08375	Oligonucleotide 17
C	39	15.2	42.2	61	22	AAAS08375	plg_PHGXP 3' UTR c
C	40	15.2	42.2	75	20	AAAV3628	Hair pin-like struc
C	41	15	41.7	25	22	AAAX28151	Universal adaptor
C	42	15	41.7	49	16	AAAT63075	Human PPT-1 gene e
C	43	15	41.7	51	22	AAAL31737	Primer 1 for amplifi
C	44	15	41.7	51	22	AAAT77604	Human SNP oligonuc
C	45	15	41.7	51	22	AAAT77606	Human silent SNP c

ALIGNMENTS

RESULT	1
AA086648	
ID	AA086648 standard; DNA; 36 BP.
XX	
AC	AA086648;
XX	
DT	27-SEP-1995 (first entry)
XX	
DE	Bcl-2 splice acceptor site.
XX	
XX	Anticodc oligomer; antisense oligonucleotide; bcl-2; cancer; therapy
XX	leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KN	ss.
XX	
OS	Synthetic.
XX	
PN	WO9508350-A.
XX	
PD	30-MAR-1995.
XX	
PE	20-SEP-1994; 94WO-US10725.
XX	
PR	20-SEP-1993; 93US-0124256.
XX	
PA	(REED/) REED J C.
XX	
PI	Reed JC;
XX	
DR	WPI; 1995-139394/18.
XX	
PT	Anti-codc oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer

XX PS Disclosure; Page 13: 108pp; English.
 CC CC The antisense oligonucleotide SA-AS (AA086647) is complementary to a
 CC portion of the splice acceptor site of the pre-mRNA coding strand of
 CC the human bcl-2 gene. It reduces the expression of bcl-2 gene product,
 CC thereby inducing programmed cell death of certain cancer cells. The
 CC corresp. bcl-2 sense splice acceptor site region was synthesized for
 CC use as a control.
 XX

SQ Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 36; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 ccccaactgcagatgctcttggtaactgtacg 36
 ||||||||||||||||||||||||||||
 Db 1 ccccaactgcagatgctcttggtaactgtacg 36

RESULT 2

ID AAV19656 standard; DNA; 36 BP.

AAV19656;

12-JUN-1998 (first entry)

Human bcl-2 oligonucleotide 3.

Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

cancer; ss.

Synthetic.

Homo sapiens.

US5734033-A.

31-MAR-1998.

24-MAR-1994; 94US-0288692.

21-FEB-1992; 92US-0840716.

22-DEC-1988; 88US-0288692.

24-MAR-1994; 94US-0217082.

(UYPE-) UNTV PENNSYLVANIA.

Reed J;

WPI; 1998-229881/20.

Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

Disclosure: Columns 3-4; 21pp; English.

XX This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the splice acceptor site of the human
 CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.

SQ Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 36; DB 19; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 ccccaactgcagatgctcttggtaactgtacg 36
 ||||||||||||||||||||||||||||
 Db 1 ccccaactgcagatgctcttggtaactgtacg 36

RESULT 3

AA051962 standard; RNA; 34 BP.

AA051962;

26-MAY-1994 (first entry)

BCL-2 mRNA ribozyme cleavable nucleotide (2043).

Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 human; chronic myelogenous leukemia; CML; follicular lymphoma;
 B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 hairpin; hepatitis delta virus; group I intron; RNaseP, ss.

Homo sapiens.

WO9323057-A.

25-NOV-1993.

13-MAY-1993; 93WO-US04573.

14-MAY-1992; 92US-0882822.

14-MAY-1992; 92US-0882885.

26-AUG-1992; 92US-0936110.

26-AUG-1992; 92US-0936421.

26-AUG-1992; 92US-0936422.

26-AUG-1992; 92US-0936531.

26-AUG-1992; 92US-0936532.

07-DEC-1992; 92US-0987131.

19-JAN-1993; 93US-0006122.

19-JAN-1993; 93US-0008910.

(RIBO-) RIBOZYME PHARM INC.

Draper KG, Thompson JD;

WPI; 1993-386203/48.

New enzymatic RNA molecules (ribozymes) - which cleave mRNA
 associated with tumours or mRNA expressed from gene encoding
 multiple drug resistance

Claim 3; Fig 6; 69pp; English.

XX The sequences given in AA051825-2266 represent areas of mRNAs which are
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed

OS Synthetic.
OS Homo sapiens.
XX
XX MO9823742-A1.
XX
XX
XX 04-JUN-1998.
XX
XX
XX 18-NOV-1997; 97WO-GB03159.
XX
XX 03-OCT-1997; 97GB-0020995.
XX 25-NOV-1996; 96GB-0024442.
XX
XX (MERT) MERCK SHARP & DOHME LTD.
XX
XX Whiting PJ;
XX WPI; 1998-322722/28.
XX
XX
XX New isolated GABA receptor subunit, epsilon - used to develop
PT products for the screening and design of drugs, e.g. for modulating
PT appetite behaviours, hormonal interactions and cognition
XX
XX Example 3; Page 20; 37pp; English.
XX
XX Antisense oligonucleotide probes 1 and 2 (see AAV36325) are based
CC on human GABA receptor novel epsilon subunit cDNA (see AAV36319).
CC Each was radiolabelled at the 3' end with (35S)deoxyadenosine
CC 5'-(thiotriphosphate) and used in in situ hybridisation assays
CC to localise the epsilon subunit in monkey brain. The localisation
CC appeared to be very restricted, residing mainly in the hypothalamus
CC and arcuate nucleus. The new GABA receptor epsilon subunit (see
CC AAW61045) can be used in the screening and design of drugs which act
CC on the GABA receptor and which may be useful e.g. for the modulation
CC of appetite behaviours, hormonal interactions and cognition.
XX
XX Sequence 45 BP; 9 A; 13 C; 11 G; 12 T; 0 other;
SQ

Query Match 47.2%; Score 17; DB 19; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 cccccaactgcagatgccttctgt 25
DB 6 ccgcacaactcaggaagcttctgt 30

RESULT 7
AAI79508
ID AAI79508 standard; DNA; 51 BP.
XX
XX AAI79508;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:6449.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
XX 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
PA

XX
XX Shinkets RA, Leach M;
PI
XX
XX WPI; 2001-356160/37.
DR
XX
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
PT
XX
XX Claim 1; Page 2481; 2653pp; English.
XX
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
XX Sequence 51 BP; 10 A; 18 C; 12 G; 11 T; 0 other;
SQ

Query Match 46.7%; Score 16.8; DB 22; Length 51;
Best Local Similarity 66.7%; Pred. NO. 1.4e+03;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 cccccaactgcagatgccttctgtgactgtacg 36
DB 10 ccaccaactgcgtcatcttgcagactcgtcg 45

RESULT 8
AAI79509
ID AAI79509 standard; DNA; 51 BP.
XX
XX AAI79509;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:6450.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
XX 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
PI
XX
XX WPI; 2001-356160/37.
DR
XX

PT polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
PS Claim 1; Page 2481; 2653pp; English.
XX
XX
CC AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The presence of polymorphic polypeptides in samples.
XX
XX
SQ Sequence 51 BP; 10 A; 19 C; 12 G; 10 T; 0 other;
XX
XX
Query Match 46.7%; Score 16.8; DB 22; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ccccaactgcagatccttctgtgaactgtacg 36
||| ||||| ||| ||| |||
Db 10 ccacacactgcctgcacaccttgacactcgtcg 45
XX
XX
RESULT 9
ID AAA72693 standard; DNA; 47 BP.
XX
XX AAA72693;
AC
DT 08-DEC-2000 (first entry)
XX
XX PCR primer used for Crt gene isolation.
DE
XX
XX Polyhydroxyalkanoate; PHA; polyhydroxybutyrate; PHB; moulding; bottle;
KM cosmetic container; nappy sheet; pen; golf tee; tampon applicator;
KM PCR primer; Crt; PHB; ss.
XX
XX Clostridium acetobutylicum.
OS
XX
XX WO200043523-A2.
PN
XX
XX 27-JUL-2000.
PD
XX
XX 21-JAN-2000; 2000WO-US01526.
PF
XX
XX 22-JAN-1999; 99US-0235875.
PR
XX
XX (META-) METABOLIX INC.
PA
XX
XX Madison L, Huisman GW, Peoples OP;
PI
XX
XX WPI; 2000-505840/45.
DR
XX
XX Stable and efficient biological production of polyhydroxyalkanoates
PT (PHA) containing 3-hydroxyhexanoate, comprising synthesis in transgenic
PT organisms with transgene(s) encoding enzymes e.g. PHA polymerase -
XX
XX
XX Example 3; Page 22; 48pp; English.

CC This invention relates to methods for the production of
CC polyhydroxyalkanoates (PHAs) containing 3-hydroxyhexanoate. The method
CC comprises synthesizing the PHA in a transgenic organism with at least 1
CC transgene encoding an enzyme. The enzyme is chosen from
CC polyhydroxybutyrate (PHB) polymerase, PHA polymerase, beta-ketothiolase,
CC beta-ketoadyl-coenzyme A (CoA) reductase, D-specific enoyl-CoA hydratase,
CC crotonase, butyryl-CoA dehydrogenase and 3-hydroxybutyryl-CoA
CC dehydrogenase integrated into the chromosome. The method is used for the
CC biological production of polyhydroxyalkanoates containing
CC 3-hydroxyhexanoate, which are useful in moulding applications
CC particularly consumer packaging items such as bottles, cosmetic
CC containers, nappy sheets, pens, golf tees and personal items such as
CC moulded tampon applicators. They provide genetically engineered systems
CC for the production of polyhydroxyalkanoates containing
CC 3-hydroxyhexanoates. They are used to provide useful mutations that can
CC be used to produce 3-hydroxyhexanoic monomers from more economic
CC feedstocks, such as butyrate or butanol. They are used to provide genes
CC suitable for converting cellular metabolites derived from carbohydrate
CC feedstocks to butyryl-CoA for the production of 3-hydroxyhexanoate
CC co-monomers. The present sequence represents a PCR primer used to isolate
CC the Crt gene. The PCR product is used in a method for the synthesis of
CC PHB.
XX
XX
SQ Sequence 47 BP; 14 A; 8 C; 12 G; 13 T; 0 other;
XX
XX
Query Match 46.1%; Score 16.6; DB 21; Length 47;
Best Local Similarity 71.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 4 ccaactgcagatgccttctgtgaactgtac 34
||| ||||| ||| ||| |||
Db 7 ccgaattcaggaaggtttttagaactaac 37
XX
XX
RESULT 10
ID AAC63894 standard; DNA; 40 BP.
XX
XX AAC63894;
AC
DT 09-FEB-2001 (first entry)
XX
XX Chinese hamster/rat beta-actin PCR primer, SEQ ID NO:6.
DE
XX
XX Immunologically functional molecule; immune system; immunomodulation;
KM glycosylation; fucose; N-acetylglucosamine; cancer; circulatory disease;
KM viral infection; bacterial infection; allergy; autoimmune disease;
KM inflammation; antibody; Chinese hamster; rat; beta-actin PCR primer; ss.
XX
XX Cricetus griseus.
OS
XX
XX Rattus sp.
OS
XX
XX WO200061739-A1.
PN
XX
XX 19-OCT-2000.
PD
XX
XX 07-APR-2000; 2000WO-JP02260.
PF
XX
XX 09-APR-1999; 99JP-0103158.
PR
XX
XX (KYOWA) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Nakamura K, Shoji E, Yamasaki M, Uchida K, Shinkawa T;
PI Imadeppu S, Kanda Y, Yamane N, Anazawa H;
PI
XX
XX WPI; 2000-665129/64.
DR
XX
XX Control of activity of antibodies and other immunologically functional
PT molecules by addition or removal of fucose from sugar chain for
PT diagnosis and treatment of cancer, allergy and other diseases -
XX
XX
XX Example 8; Page 74; 81pp; Japanese.

XX The invention relates to a method for controlling the activity of an
 CC immunologically functional molecule (e.g., an antibody) where the
 CC control is effected by the presence or absence of a sugar bound to an
 CC N-acetylglucosamine residue at the reducing end of the sugar chain on
 CC the immunologically functional molecule. The invention also relates to
 CC methods for the diagnosis, prevention or treatment of diseases which
 CC involve the modified immunologically functional molecule, and agents
 CC which stimulate the activity of an immunologically functional molecule.
 CC The methods of the invention are used for the diagnosis, treatment and
 CC prevention of a broad range of diseases including cancer, circulatory
 CC disease, viral or bacterial infection, allergy, autoimmune disease and
 CC inflammation. The present sequence represents a Chinese hamster/rat
 CC beta-actin PCR primer used in an exemplification of the invention.
 XX
 SQ Sequence 40 BP; 10 A; 5 C; 16 G; 9 T; 0 other;

Query Match 45.0%; Score 16.2; DB 21; Length 40;
 Best Local Similarity 85.7%; Pred. No. 2.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 aactgcagagtgcttgg 26
 |||||
 Db 5 aactgcagagtgcttgg 25

RESULT 11
 AA237381/C
 ID AA237381 standard; DNA; 20 BP.
 XX

AC AA237381;

DT 04-FEB-2000 (first entry)

DE PCR primer for human Bcl-2 gene.

XX Bcl-2; human; PCR primer; adenoviral vector; anti-apoptotic gene;
 KW Ischaemia; reperfusion injury; liver; organ preservation;
 KM endothelial cell cryoprotection; ss.
 XX

OS Synthetic.

OS Homo sapiens.

PN WO955382-A1.

PD 04-NOV-1999.

PF 29-APR-1999; 99WO-US09412.

PR 29-APR-1998; 98US-0083434.

PA (UABR-) UAB RES FOUND.

PI Bilbao G, Curriel DT, Contreras JL;

DR WPI: 2000-023269/02.

PT Adenoviral vector encoding anti-apoptotic Bcl-2 gene useful for
 PT cytoprotection and in gene therapy -

PS Example 9; Page 26; 89pp; English.

CC This sequence represents a PCR primer for the human Bcl-2 gene. The
 CC invention relates to an adenoviral vector encoding an anti-apoptotic
 CC Bcl-2 gene. The adenoviral vector may be used to reduce
 CC ischaemia/reperfusion injury in the liver, improve organ preservation,
 CC cytoprotect endothelial cells or pancreatic islet cells during cold
 CC preservation, or enhance or prolong the expression of a transgene. The
 CC expression of Bcl-2 with a transgene mediated a significant reduction
 CC in apoptosis and necrosis following adenovirus mediated gene transfer,
 CC and an enhancement of transgene expression (up to 2 log).

SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 other;

Query Match 44.4%; Score 16; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 ttgtggaactgtgaag 36
 |||||
 Db 20 TTGTGGAACGTGACG 5

RESULT 12
 AA114539
 ID AA114539 standard; DNA; 34 BP.
 XX

AC AA114539;

DT 10-SEP-1996 (first entry)

DE Fc receptor PCR primer LR3.

XX Fc receptor; Fc gamma RI; Fc epsilon RI; IgE; autoimmune disease;
 KW therapy; polymerase chain reaction; PCR; primer; ss.
 XX

OS Synthetic.

PN WO9608512-A1.

PD 21-MAR-1996.

PF 15-SEP-1995; 95WO-AU00606.

PR 31-OCT-1994; 94US-0332562.

PR 16-SEP-1994; 94AU-0008232.

PA (AUST-) AUSTIN RES INST CANCER & ANTI INFLAMMATORY SYNDICATE NO.1.

PI Baker RI, Hogarth PM, Hulett MD, McKenzie IFC, Powell MS;

DR WPI: 1996-179903/18.

XX New mutant Fc receptor polypeptide(s) - have amino acid changes to
 PT improve characteristics, e.g. half life, used partic in diagnosis or
 PT treatment of auto-immune diseases
 XX

PS Example 5; Page 48; 104pp; English.

CC Antisense PCR primer LR3 (AA114539) was used with sense primer NR1
 CC (AA114531) and with primer pair LR4 + EG5 (AA114540 + AA114532) to
 CC construct cDNA coding for chimeric receptor CC', comprising a
 CC receptor with domain 1 from Fc gamma RI, domain 2 from Fc
 CC epsilon RI, a transmembrane region from Fc gamma RI and the CC'
 CC loop from Fc epsilon RI. The chimeric receptor was expressed by
 CC transfected COS monolayers. Rosetting assays showed that the
 CC transfected cells rosetted less well than either transfectants
 CC (see also AA114537-38 and AA114541-42).
 XX

SQ Sequence 34 BP; 6 A; 11 C; 8 G; 9 T; 0 other;

Query Match 43.9%; Score 15.8; DB 17; Length 34;
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 11 cagatgcttgggaac 29
 |||||
 Db 13 caggtgtcattgtggaac 31

RESULT 13
 AA90551
 ID AA90551 standard; cDNA; 36 BP.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:43 ; Search time 334.55 Seconds
(without alignments)
26.432 Million cell updates/sec

Title: US-09-709-170A-6

Perfect score: 36
Sequence: 1 cccccacgcagatgccttctgtgaactgtacgg 36

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	1	US-08-217-082A-6 Sequence 6, Appli
2	36	100.0	36	2	US-08-465-485A-6 Sequence 6, Appli
3	36	100.0	36	3	US-09-080-285-6 Sequence 6, Appli
4	24	66.7	34	1	US-07-936-421-16 Sequence 16, Appli
5	20	55.6	20	1	US-08-217-082A-5 Sequence 5, Appli
6	20	55.6	20	2	US-08-465-485A-5 Sequence 5, Appli
7	20	55.6	20	3	US-09-080-285-5 Sequence 5, Appli
8	15.4	42.8	30	4	US-09-053-871A-4 Sequence 4, Appli
9	15.4	42.8	31	4	US-09-053-871A-5 Sequence 4, Appli
10	15.4	42.8	32	4	US-09-053-871A-6 Sequence 5, Appli
11	15.2	42.2	20	3	US-09-288-461-83 Sequence 83, Appli
12	15.2	42.2	20	4	US-09-167-921-35 Sequence 35, Appli
13	15.2	42.2	20	4	US-09-277-020-46 Sequence 46, Appli
14	15.2	42.2	20	4	US-09-323-743-35 Sequence 35, Appli
15	15.2	42.2	27	3	US-08-513-974B-87 Sequence 87, Appli
16	15.2	42.2	30	4	US-09-053-871A-20 Sequence 20, Appli
17	15.2	42.2	40	2	US-08-425-684-19 Sequence 19, Appli
18	15.2	42.2	40	2	US-08-675-502-19 Sequence 19, Appli
19	15.2	42.2	60	2	US-08-663-566A-47 Sequence 47, Appli
20	15.2	42.2	60	2	US-08-023-610-47 Sequence 47, Appli
21	15.2	42.2	60	2	US-08-288-065A-47 Sequence 47, Appli
22	15.2	42.2	60	2	US-08-362-240A-47 Sequence 47, Appli
23	15.2	42.2	60	5	PCT-US95-10245-47 Sequence 47, Appli
24	15.2	42.2	63	3	US-08-969-320-1 Sequence 1, Appli
25	15	41.7	49	4	US-08-718-388-10 Sequence 10, Appli
26	15	41.7	54	1	US-08-484-686B-25 Sequence 25, Appli
27	15	41.7	54	4	US-08-463-160B-25 Sequence 25, Appli

28	15	41.7	54	5	PCT-US91-02568-26 Sequence 26, Appli
29	14.8	41.1	38	1	US-08-358-810A-1 Sequence 1, Appli
30	14.8	41.1	38	1	US-08-484-712A-1 Sequence 1, Appli
31	14.8	41.1	38	1	US-08-359-295C-3 Sequence 3, Appli
32	14.8	41.1	38	1	US-08-659-453B-5 Sequence 5, Appli
33	14.8	41.1	38	2	US-08-485-105A-3 Sequence 3, Appli
34	14.8	41.1	38	3	US-09-089-853A-5 Sequence 5, Appli
35	14.8	41.1	38	3	US-09-183-650-3 Sequence 3, Appli
36	14.8	41.1	38	3	US-09-196-543D-5 Sequence 5, Appli
37	14.8	41.1	38	4	US-09-131-009A-5 Sequence 5, Appli
38	14.8	41.1	38	4	US-09-092-226A-5 Sequence 5, Appli
39	14.8	41.1	38	4	US-09-269-911A-3 Sequence 3, Appli
40	14.8	41.1	38	4	US-09-130-862A-5 Sequence 5, Appli
41	14.8	41.1	38	4	US-09-090-809A-5 Sequence 5, Appli
42	14.8	41.1	38	4	US-09-053-116A-5 Sequence 5, Appli
43	14.8	41.1	45	1	US-08-291-299-3 Sequence 3, Appli
44	14.8	41.1	45	5	PCT-US95-10579-3 Sequence 3, Appli
45	14.6	40.6	71	4	US-09-363-939A-38 Sequence 38, Appli

ALIGNMENTS

RESULT 1
US-08-217-082A-6
Sequence 6, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
NUMBER OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-6

Query Match 100.0%; Score 36; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccccaactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 ccccaactgcagatgccttctgtggaactgtacg 36

RESULT 2

US-08-465-485A-6
; Sequence 6, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-6

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccccaactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 ccccaactgcagatgccttctgtggaactgtacg 36

RESULT 3
US-09-080-285-6
; Sequence 6, Application US/09080285

Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-6

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccccaactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 ccccaactgcagatgccttctgtggaactgtacg 36

RESULT 4
US-07-936-421-16
; Sequence 16, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; NUMBER OF SEQUENCES: 22

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/936,421
;; FILING DATE: 19920826
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: none
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION/DOCKET NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 197/243
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-07-936-421-16

Query Match 66.7%; Score 24; DB 1; Length 34;
Best Local Similarity 70.8%; Pred. No. 0.22;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 13 ggaatccttggaactgacg 36
|||||:|||||:|||||
Db 1 GGAUGCCUUGGAGACUGACG 24

RESULT 5
US-08-217-082A-5/C
; Sequence 5, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/840,716
;; FILING DATE: 21-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/288,692
;; FILING DATE: 22-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fortney, Andrew D.
;; REGISTRATION NUMBER: 34,600
;; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (408) 436-2070
;; TELEFAX: (408) 436-2075
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: Synthetic DNA
;; ANTI-SENSE: YES
;; US-08-217-082A-5

Query Match 55.6%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcagatgccttgt 24
|||||:|||||:|||||
Db 20 CAACGACAGATGCTTGTG 1

RESULT 6
US-08-465-485A-5/C
; Sequence 5, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-5

Query Match 55.6%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 caactgcagatgccttctgt 24
|||||
DB 20 CAACTGCAGATGCCTTGT 1

RESULT 7
US-09-080-285-5/C
Sequence 5, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES
US-09-080-285-5

Query Match 55.6%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 caactgcagatgccttctgt 24
|||||
DB 20 CAACTGCAGATGCCTTGT 1

RESULT 8
US-09-053-871A-4/C
Sequence 4, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing Factor IXm.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-4

Query Match 42.8%; Score 15.4; DB 4; Length 30;
Best Local Similarity 67.9%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 actgcagatgccttctgtggaactgtac 34
|||||
DB 28 ACCCGAGGGGNNNTAGAGGAACTGTAC 1

RESULT 9
US-09-053-871A-5/C
Sequence 5, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing Factor IXm1.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-5

Query Match 42.8%; Score 15.4; DB 4; Length 31;
Best Local Similarity 67.9%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 7 actgacagatgacctgtgtgacctgtac 34
|| ||||| | | |||||
Db 28 ACCCAGGGGNNNTAGAGAACTGTAC 1

RESULT 10
US-09-053-871A-6/c
Sequence 6, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
TITLE OF INVENTION: STROKE OUTCOME
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053, 871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing Factor IXm1.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-6

Query Match 42.8%; Score 15.4; DB 4; Length 32;
Best Local Similarity 67.9%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 7 actgacagatgacctgtgtgacctgtac 34
|| ||||| | | |||||
Db 28 ACCCAGGGGNNNTAGAGAACTGTAC 1

RESULT 11
US-09-288-461-83/c
Sequence 83, Application US/09288461
Patent No. 6159694
GENERAL INFORMATION:
APPLICANT: Karas, James G.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0338
CURRENT APPLICATION NUMBER: US/09/288, 461
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 83
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence

US-09-288-461-83

Query Match 42.2%; Score 15.2; DB 3; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 gcagagatgacctgtgtgacctgtac 29
|| ||||| | | |||||
Db 20 GCAGAGATGCTCAGTGGAC 1

RESULT 12
US-09-167-921-35/c
Sequence 35, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167, 921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-167-921-35

Query Match 42.2%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 gatcctgtgtgacctgtac 33
|| | ||||| |||||
Db 20 GATCCTTTTGTGAACTCTA 1

RESULT 13
US-09-277-020-46/c
Sequence 46, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277, 020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167, 921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 46
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-46

Query Match 42.2%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 14 gatgccttcttggaactgta 33
||| | ||||| ||||| ||
Db 20 GATACCTTTTGTGGAACCTCTA 1

RESULT 14

US-09-323-743-35/C
; Sequence 35, Application US/09323743
; Patent No. 6214986
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, Qinqiong
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0368
; CURRENT APPLICATION NUMBER: US/09/323,743
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 09/277,020
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-323-743-35

Query Match 42.2%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 14 gatgccttcttggaactgta 33
||| | ||||| ||||| ||
Db 20 GATACCTTTTGTGGAACCTCTA 1

RESULT 15

US-08-513-974B-87
; Sequence 87, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-87

Query Match 42.2%; Score 15.2; DB 3; Length 27;
Best Local Similarity 85.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 caactgcagatgccttctgt 24
||| | ||||| ||||| ||
Db 6 CATCTGCTGATGCCTTCT 25

Search completed: June 28, 2002, 22:16:44
Job time: 8270 sec

Mon Jul 1 08:40:58 2002

us-09-709-170a-6.szlm75.rni

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:01 ; Search time 3762.88 Seconds
(without alignments)
111.226 Million cell updates/sec

Title: US-09-709-170A-7
Perfect score: 20
Sequence: 1 gggagagatggcgacacgctg 20

Scoring table:
IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htgo.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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c	1	20	100.0	20	6	AR052603	AR052603 Sequence
c	2	20	100.0	20	6	AR052609	AR052609 Sequence
c	3	20	100.0	20	6	AR176022	AR176022 Sequence
c	4	20	100.0	20	6	AR176023	AR176023 Sequence
c	5	20	100.0	20	6	AX211659	AX211659 Sequence
c	6	20	100.0	20	6	AX211670	AX211670 Sequence
c	7	20	100.0	20	6	AX277461	AX277461 Sequence
c	8	20	100.0	20	6	196082	196082 Sequence 1
c	9	20	100.0	20	6	196088	196088 Sequence 7
c	10	20	100.0	22	6	A76123	A76123 Sequence 3
c	11	20	100.0	22	6	A76124	A76124 Sequence 4
c	12	20	100.0	35	6	AR052604	AR052604 Sequence
c	13	20	100.0	35	6	196083	196083 Sequence 2
c	14	18	95.0	20	6	AX045387	AX045387 Sequence
c	15	18	90.0	18	6	BD008994	BD008994 Inhibitor
c	16	17	85.0	17	6	196092	196092 Sequence 11
c	17	16	80.0	17	6	196091	196091 Sequence 10
c	18	15.8	79.0	51	6	AX165740	AX165740 Sequence
c	19	15.4	77.0	29	5	CHRC2A101	K02260 Chicken alp
c	20	15	75.0	15	6	AX277468	AX277468 Sequence
c	21	15	75.0	15	6	AX277469	AX277469 Sequence
c	22	15	75.0	17	6	196093	196093 Sequence 12
c	23	14	70.0	19	6	AX083694	AX083694 Sequence
c	24	13.8	69.0	50	6	AX113707	AX113707 Sequence
c	25	13.8	69.0	60	6	AX113708	AX113708 Sequence
c	26	13.8	69.0	70	6	AX113709	AX113709 Sequence
c	27	13.6	68.0	27	6	AR004426	AR004426 Sequence
c	28	13.6	68.0	27	6	143661	143661 Sequence 13
c	29	13.6	68.0	27	6	186720	186720 Sequence 8
c	30	13.4	67.0	24	6	AX290202	AX290202 Sequence
c	31	13.2	66.0	47	6	AR153764	AR153764 Sequence
c	32	13.2	66.0	47	6	AR153766	AR153766 Sequence
c	33	13.2	66.0	51	6	AX157777	AX157777 Sequence
c	34	13.2	66.0	51	6	AX157778	AX157778 Sequence
c	35	13.2	66.0	51	6	AX157779	AX157779 Sequence
c	36	13	65.0	16	6	AX103898	AX103898 Sequence
c	37	13	65.0	16	6	AX355505	AX355505 Sequence
c	38	13	65.0	17	6	196090	196090 Sequence 9
c	39	13	65.0	18	6	AR052619	AR052619 Sequence
c	40	13	65.0	18	6	AR052624	AR052624 Sequence
c	41	13	65.0	18	6	AR116926	AR116926 Sequence
c	42	13	65.0	18	6	AR140926	AR140926 Sequence
c	43	13	65.0	18	6	AR146347	AR146347 Sequence
c	44	13	65.0	18	6	AR146392	AR146392 Sequence
c	45	13	65.0	18	6	AR154716	AR154716 Sequence

ALIGNMENTS

RESULT 1
AR052603/c AR052603 20 bp DNA
LOCUS AR052603
DEFINITION Sequence 1 from patent US 5831066.
ACCESSION AR052603
VERSION AR052603.1 GI:5975967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A1 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best local similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
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Db 20 GGGAAGATGGCGCAGCTG 1

RESULT 2
AR052609
LOCUS AR052609 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5831066.
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
|||||
Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 3
AR176022/c
LOCUS AR176022 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GGGAAGATGGCGCAGCTG 1

RESULT 4
AR176023
LOCUS AR176023 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023

VERSION AR176023.1 GI:17917322
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
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Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 5
AX211669
LOCUS AX211669 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 1 from Patent WO0159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatt,S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
Yissum Research Development Co., The Hebrew University of Jerusalem (IL)

FEATURES Location/Qualifiers
SOURCE 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="..."

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
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Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 6
AX211670/c
LOCUS AX211670 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 2 from Patent WO0159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatt,S.

TITLE Detection of binding of charged species using ph- or
potential-sensitive probes

JOURNAL Patent: WO 0159156-A 2 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem
(II)

FEATURES Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
|||||
Db 20 GGGAGAGATGGCGACGCTG 1

RESULT 7
AX277461/c AX277461 20 bp DNA linear PAT 29-OCT-2001
LOCUS Sequence 1 from Patent WO0160998.
DEFINITION AX277461
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (sites)
AUTHORS Tarr, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
TITLE Small oligonucleotides with anti-tumor activity
JOURNAL Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)
Location/Qualifiers
1..20

FEATURES source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Primer"

BASE COUNT 2 a 10 c 4 g 4 t
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Db 20 GGGAGAGATGGCGACGCTG 1

RESULT 8
196082/c 196082 20 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 1 from patent US 5734033.
DEFINITION 196082
ACCESSION 196082
VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
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Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GGGAGAGATGGCGACGCTG 1

RESULT 9
196088 196088 20 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 7 from patent US 5734033.
DEFINITION 196088
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
1..20
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BASE COUNT 4 a 4 c 10 g 2 t
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
|||||
Db 1 GGGAGAGATGGCGACGCTG 20

RESULT 10
A76123/c A76123 22 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 3 from Patent W09320200.
DEFINITION A76123
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 3 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERRARD IAN (GB)
Location/Qualifiers
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BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
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Db 22 GGGAGAGATGGCGACGCTG 3

RESULT 11
A76124/c 22 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 4 from Patent WO9320200.
DEFINITION A76124
ACCESSION A76124
VERSION A76124.1 GI:6088260
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan,G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
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BASE COUNT 2 a 12 c 4 g 4 t
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RESULT 12
AR052604 35 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 2 from patent US 5831066.
DEFINITION AR052604
ACCESSION AR052604
VERSION AR052604.1 GI:5975968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;
FEATURES location/Qualifiers
source 1..35
/organism="unknown"
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

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Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 13
I96083 35 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 2 from patent US 5734033.
DEFINITION I96083
ACCESSION I96083
VERSION I96083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES location/Qualifiers
source 1..35
/organism="unknown"
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggaagatgagcagctg 20
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 14
AX045387/c 20 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 7 from Patent WO0066724.
DEFINITION AX045387
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE bcl-2 mRNA
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense"
BASE COUNT 2 a 10 c 4 g 4 t
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Best Local Similarity 100.0%; Pred. No. 1,5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ggaagatgagcagctg 20
Db 20 GGGAAGATGGCGCAGCTG 2

RESULT 15
BD008994/c 18 bp DNA linear PAT 31-JAN-2002
LOCUS Inhibition of bcl-2 protein expression by liposomal antisense
DEFINITION BD008994
ACCESSION BD008994
VERSION BD008994.1 GI:18637367
KEYWORDS JP 2001502172-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Tormo,M., Tara,A.M., Berestein,G.L. and McDonnell,T.J.
TITLE Inhibition of bcl-2 protein expression by liposomal antisense
JOURNAL Patent: JP 2001502172-A 1 20-FEB-2001.
COMMENT BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
OS Unidentified

PN JP 2001502172-A/1
 PD 20-FEB-2001
 PE 03-OCT-1997 JP 1998516985
 PR 04-OCT-1996 US 08/726211
 PI MAR TORMO, ANA M TARA, GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
 MCDONNELL

PC A61K9/127, A61K31/70, C07H21/04, C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH key Location/Qualifiers
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 FT source Location/Qualifiers

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:32644"

BASE COUNT 2 a 8 c 4 g 4 t
 ORIGIN

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gaagagatggcgacagctg 20
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 Db 18 GAAGGATGGCGACAGCTG 1

Search completed: June 28, 2002, 22:11:03
 Job time: 8354 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:44 ; Search time 334.55 seconds
(without alignments)
14.664 Million cell updates/sec

Title: US-09-709-170A-7

Perfect score: 20

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Scoring table: IDENTITY_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
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1	20	100.0	20	1	US-08-217-082A-1	Sequence 1, Appl
2	20	100.0	20	1	US-08-217-082A-7	Sequence 7, Appl
3	20	100.0	20	2	US-08-465-485A-1	Sequence 1, Appl
4	20	100.0	20	2	US-08-465-485A-7	Sequence 7, Appl
5	20	100.0	20	3	US-09-080-285-1	Sequence 1, Appl
6	20	100.0	20	3	US-09-080-285-7	Sequence 7, Appl
7	20	100.0	20	4	US-09-379-718-1	Sequence 1, Appl
8	20	100.0	20	4	US-09-379-718-2	Sequence 2, Appl
9	20	100.0	35	1	US-08-217-082A-2	Sequence 1, Appl
10	20	100.0	35	2	US-08-465-485A-2	Sequence 2, Appl
11	20	100.0	35	3	US-09-080-285-2	Sequence 2, Appl
12	17	85.0	17	1	US-08-217-082A-11	Sequence 11, Appl
13	16	80.0	17	1	US-08-217-082A-10	Sequence 10, Appl
14	15	75.0	17	1	US-08-410-804-12	Sequence 12, Appl
15	13	68.0	27	1	US-08-410-804-13	Sequence 13, Appl
16	13	68.0	27	1	US-08-607-269-8	Sequence 8, Appl
17	13	68.0	27	1	US-08-259-514-13	Sequence 13, Appl
18	13	68.0	27	2	US-08-858-311-13	Sequence 13, Appl
19	13	68.0	27	5	PCT-US95-04600-8	Sequence 8, Appl
20	13	66.0	47	4	US-08-869-380-5	Sequence 5, Appl
21	13	66.0	47	4	US-08-869-380-7	Sequence 7, Appl
22	13	66.0	47	5	PCT-US95-13552-16	Sequence 16, Appl
23	13	66.0	47	5	PCT-US95-13552-18	Sequence 18, Appl
24	13	65.0	17	1	US-08-217-082A-9	Sequence 9, Appl
25	13	65.0	18	1	US-08-217-082A-17	Sequence 17, Appl
26	13	65.0	18	2	US-08-465-485A-17	Sequence 17, Appl
27	13	65.0	18	2	US-08-465-485A-24	Sequence 24, Appl

C 28	13	65.0	18	3	US-09-080-285-17	Sequence 17, Appl
C 29	13	65.0	18	3	US-09-080-285-24	Sequence 24, Appl
C 30	13	65.0	18	3	US-09-249-730-218	Sequence 218, App
C 31	13	65.0	18	3	US-09-118-220-1	Sequence 1, Appl
C 32	13	65.0	18	4	US-08-738-652-55	Sequence 55, Appl
C 33	13	65.0	18	4	US-09-030-701-27	Sequence 27, Appl
C 34	13	65.0	18	4	US-09-286-098-59	Sequence 59, Appl
C 35	13	65.0	18	4	US-09-286-098-104	Sequence 104, App
C 36	13	65.0	18	4	US-08-960-774-45	Sequence 45, Appl
C 37	13	65.0	19	4	US-09-078-934-14	Sequence 14, Appl
C 38	13	65.0	19	6	5276019-8	Patent No. 5276019
C 39	13	65.0	20	4	US-09-082-649B-60	Sequence 60, Appl
C 40	12	64.0	20	3	US-09-418-640-84	Sequence 84, Appl
C 41	12	63.0	32	4	US-09-272-496-5	Sequence 5, Appl
C 42	12	62.0	45	4	US-08-358-627F-1	Sequence 1, Appl
C 43	12	62.0	21	4	US-09-485-636-25	Sequence 25, Appl
C 44	12	61.0	30	5	PCT-US94-10257A-37	Sequence 37, Appl
C 45	12	61.0	33	3	US-08-816-346-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-08-217-082A-1/C

Sequence 1, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 224 Airport Parkway

CITY: San Jose

STATE: California

COUNTRY: U.S.A.

ZIP: 95110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,082A

FILING DATE: 24-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: Synthetic DNA

ANTI-SENSE: YES

US-08-217-082A-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggagagatgagcagcagctg 20
|||||
Db 20 GGGAGAGATGGCGCACGCTG 1

RESULT 2
US-08-217-082A-7
; Sequence 7, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: NO
US-08-217-082A-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGAGAGATGGCGCACGCTG 20

RESULT 3
US-08-465-485A-1/C
; Sequence 1, Application US/08465485A

; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-1

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggagagatgagcagcagctg 20
|||||
Db 20 GGGAGAGATGGCGCACGCTG 1

RESULT 4
US-08-465-485A-7
; Sequence 7, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
DB 1 GGGAGGATGGCGACGCTG 20

RESULT 5
US-09-080-285-1/c
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
DB 20 GGGAGGATGGCGACGCTG 1

RESULT 6
US-09-080-285-7
Sequence 7, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-7

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggaagatggcgacgctg 20
|||||
DB 1 GGGGAAGATGGCGACGCTG 20

RESULT 7
US-09-379-718-1/c
Sequence 1, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
APPLICANT: Kloster, Miriam
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
FILE REFERENCE: Antisense Technology
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-1

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggaagatggcgacgctg 20
|||||
DB 20 GGGGAAGATGGCGACGCTG 1

RESULT 8
US-09-379-718-2
Sequence 2, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
APPLICANT: Kloster, Miriam
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
FILE REFERENCE: Antisense Technology
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggggaagatggcgacgctg 20
|||||
DB 1 ggggaagatggcgacgctg 20

RESULT 9
US-08-217-082A-2
Sequence 2, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 20; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 10
US-08-465-485A-2

; Sequence 2, Application US/08465485A
; Patent No. 5831066

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 S. Jefferson Davis Hwy., Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,485A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/124,256

; FILING DATE: 20-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/840,716

; FILING DATE: 21-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/288,692

; FILING DATE: 22-DEC-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Fortney, Andrew D.

; REGISTRATION NUMBER: 34,600

; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (408) 436-2070

; TELEFAX: (408) 436-2075

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: NO

; US-08-465-485A-2

; Query Match 100.0%; Score 20; DB 2; Length 35;

; Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;

; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 11

US-09-080-285-2

; Sequence 2, Application US/09080285

; Patent No. 6040181

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 1755 S. Jefferson Davis Hwy., Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/080,285

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/465,485

; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/124,256

; FILING DATE: 20-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/840,716

; FILING DATE: 21-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/288,692

; FILING DATE: 22-DEC-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Fortney, Andrew D.

; REGISTRATION NUMBER: 34,600

; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (408) 436-2070

; TELEFAX: (408) 436-2075

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: NO

; US-09-080-285-2

; Query Match 100.0%; Score 20; DB 3; Length 35;

; Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;

; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 12

US-08-217-082A-11/C

; Sequence 11, Application US/08217082A

; Patent No. 5734033

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: 224 Airport Parkway

; CITY: San Jose

STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-11

Query Match 85.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ggaagatggcgacgc 18
|||||
DB 17 GGAAGATGGCGACGC 1

RESULT 13
US-08-217-082A-10/c
Sequence 10, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-10

Query Match 80.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 agaatggcgacgcctg 20
|||||
DB 17 AGAATGGCGCACGCTG 2

RESULT 14
US-08-217-082A-12/c
Sequence 12, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:

Mon Jul 1 08:40:59 2002

us-09-709-170a-7.szlm75.rni

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:03 ; Search time 3762.88 Seconds
(Without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170a-8

Perfect score: 17

Sequence: 1 cgcgcgcgcacctcttg 17

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 1046368293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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RESULT	1	17	100.0	17	6	AR052610	Sequence	25	AR052610	Sequence
LOCUS	AR052610	AR052610	17 bp	DNA	linear	PAT 29-SEP-1999				
DEFINITION	Sequence 8 from patent US 5831066.									
ACCESSION	AR052610									
VERSION	AR052610.1	GI:5975974								
KEYWORDS										
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	1 (bases 1 to 17)									
AUTHORS	Reed, J.C.									
TITLE	Regulation of bcl-2 gene expression									
JOURNAL	Patent: US 5831066-A 8 03-NOV-1998;									
FEATURES	Location/Qualifiers									
source	1..17									
BASE COUNT	1 a 7 c 5 g 4 t									
ORIGIN										

ALIGNMENTS

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C 44	11.2	65.9	50	6	AR148432	Sequence
C 43	11.2	65.9	50	6	AR045154	Sequence
C 42	11.2	65.9	50	6	AR160483	Sequence
C 41	11.2	65.9	37	6	AR075081	Sequence
C 40	11.2	65.9	37	6	AR075081	Sequence
C 39	11.2	65.9	33	6	AR069952	Sequence
C 38	11.2	65.9	28	6	E37205	Mouse secre
C 37	11.2	65.9	24	6	BD010808	Novel pol
C 36	11.2	65.9	21	6	AX000983	Sequence
C 35	11.2	65.9	21	6	AR084992	Sequence
C 34	11.2	65.9	21	6	AR053970	Sequence
C 33	11.2	65.9	21	6	AA2054	Sequence
C 32	11.2	65.9	20	6	BD004560	Fatty aci
C 31	11.4	67.1	75	3	HYDCNHV2	Sequence
C 30	11.4	67.1	34	6	A50157	Sequence
C 29	11.4	67.1	34	6	A49730	Sequence
C 28	11.4	67.1	33	6	A14926	Oligonucleo
C 27	11.4	67.1	31	6	AX179386	Sequence
C 26	11.4	67.1	30	6	A50153	Sequence
C 25	11.4	67.1	30	6	AX292017	Sequence
C 24	11.4	67.1	24	6	AX291629	Sequence
C 23	11.4	67.1	24	6	AX296650	Sequence
C 22	11.4	67.1	20	6	AX296650	Sequence
C 21	11.4	67.1	20	6	AX296650	Sequence
C 20	11.8	69.4	72	6	AX150235	Sequence
C 19	11.8	69.4	51	6	AX157607	Sequence
C 18	11.8	69.4	30	6	E49675	Insect cell
C 17	11.8	69.4	24	6	AX291094	Sequence
C 16	11.8	69.4	20	6	AX295727	Sequence
C 15	11.8	69.4	18	6	AR106803	Sequence
C 14	12.2	71.8	66	14	SHU09127	Suid herpes
C 13	12.2	71.8	31	6	I72670	Sequence
C 12	12.2	71.8	31	6	I72668	Sequence
C 11	12.2	71.8	31	6	I24849	Sequence
C 10	12.2	71.8	31	6	I24847	Sequence
C 9	12.8	75.3	45	6	A63054	Sequence
C 8	14	82.4	17	6	AR052611	Sequence
C 7	15	88.2	18	6	BD009122	Immunosti
C 6	15	88.2	18	6	AX355457	Sequence
C 5	15	88.2	18	6	AX103864	Sequence
C 4	15	88.2	18	6	AX103812	Sequence
C 3	15	88.2	18	6	AR154731	Sequence
C 2	15	88.2	18	6	AR146348	Sequence
C 1	17	100.0	17	6	AR052610	Sequence

Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 96;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctctg 17
|||||
Db 1 CGCGTGCACCCCTCTG 17

RESULT 2
ARI46348
LOCUS ARI46348 18 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION ARI46348
VERSION ARI46348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using immunotherapeutic oligonucleotides and cytokines
JOURNAL Patent: US 6218371-A 60 17-APR-2001;
FEATURES
Source 1. .18
Location/Qualifiers
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 3
ARI54731
LOCUS ARI54731 18 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION ARI54731
VERSION ARI54731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES
Source 1. .18
Location/Qualifiers
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 4
AX103812
LOCUS AX103812 18 bp DNA PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812

VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES
Source 1. .18
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 5
AX103864
LOCUS AX103864 18 bp DNA PAT 30-APR-2001
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES
Source 1. .18
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 6
AX355457
LOCUS AX355457 18 bp DNA PAT 06-FEB-2002
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.

TITLE Methods for enhancing antibody-induced cell lysis and treating cancer

JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source
1. .18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgcgtgcgacctct 15
|||||
Db 4 CGCGTGCACCTCT 18

RESULT 7
LOCUS BD009122 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunostimulatory nucleic acid molecules.
ACCESSION BD009122
VERSION BD009122.1 GI:18637495
KEYWORDS JP 2001503267-A/74.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
Krieg, A.M. and Kline, D.N.
Immunostimulatory nucleic acid molecules
Patent: JP 2001503267-A 74 13-MAR-2001;
JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PE 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEG, JOEL N KLINE
PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,
A61K31/70
CC
FH
FT
KEY source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/db_xref="taxon:32630"

FEATURES
source
1. .18
Location/Qualifiers
1. .18
/organism="synthetic construct"
/db_xref="taxon:32630"

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgcgtgcgacctct 15
|||||
Db 4 CGCGTGCACCTCT 18

RESULT 8
LOCUS AR052611 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES Location/Qualifiers
source
1. .17
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgcgtgcgacctct 14
|||||
Db 4 CGCGTGCACCTCT 17

RESULT 9
LOCUS A63054/C 45 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 25 from Patent WO9718308.
ACCESSION A63054
VERSION A63054.1 GI:3716918
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 45)
Ashcroft, F., Sakura, H., Ashfield, R. and Ashcroft, S.J.
K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT
Patent: WO 9718308-A 25 22-MAY-1997;
JOURNAL WEILCOMBE TRUST LIMITED AS TRUS (GB)
COMMENT Other publication AU 7583296 19970605.
FEATURES Location/Qualifiers
source
1. .45
/organism="unidentified"
/db_xref="taxon:32644"

Query Match 75.3%; Score 12.8; DB 6; Length 45;
Best Local Similarity 87.5%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ggcgtgcgacctctg 17
|||||
Db 23 GGGTGCACCTCTG 8

RESULT 10
LOCUS I24847 31 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 18 from patent US 5545816.
ACCESSION I24847
VERSION I24847.1 GI:1604717
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 31)
Ausich, R.L., Brinkhaus, F.L., Mukharji, I., Proffitt, J., Yarger, J.
Ausch, R.L., Brinkhaus, F.L., Mukharji, I., Proffitt, J., Yarger, J.
phycoene biosynthesis in genetically engineered hosts
Patent: US 5545816-A 18 13-AUG-1996;
JOURNAL Location/Qualifiers

/gene="gC"
/note="formerly named glycoprotein III; signal peptide
mutant: Allele: del10"
/codon_start=1
/product="glycoprotein C"
/protein_id="AAC54537.1"
/db_xref="GI:902040"
/translation="MASLARMULLALYAAIAAAP"
BASE COUNT 4 a 27 c 24 g 11 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 14; Length 66;
Best Local Similarity 82.4%; Pred. No. 4.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgcgtcgaccctcttg 17
||||| ||| ||
Db 14 CCGTGCATGCTCCTG 30

RESULT 15

ARI06803 18 bp DNA linear PAT 14-FEB-2001
LOCUS .
DEFINITION Sequence 51 from patent US 6107091.
ACCESSION ARI06803
VERSION ARI06803.1 GI:12821333
KEYWORDS
SOURCE .
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett,L.M.
TITLE Antisense Inhibition of G-alpha-16 expression
JOURNAL Patent: US 6107091-A 51 22-AUG-2000;
FEATURES
source 1..18
Location/Qualifiers
BASE COUNT 1 a 7 c 4 g 6 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 8.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 cgtgcgaccctcttg 17
||||| ||| |||
Db 3 CGTGCCTCTCTTG 17

Search completed: June 28, 2002, 22:11:05
Job time: 8356 sec

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86550-55) or the 5'-cap
CC region (AAQ86556-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtcgagaccctctg 17
Db 1 cgcgtcgagaccctctg 17
|||||

RESULT 2
AAV28172
ID AAV28172 standard; DNA; 17 BP.
XX
AC AAV28172;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KW Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PI WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US3284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Sriwatsa GS;
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 79; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtcgagaccctctg 17
Db 1 cgcgtcgagaccctctg 17
|||||

RESULT 3
AAV23684
ID AAV23684 standard; DNA; 17 BP.
XX
AC AAV23684;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 137.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PI WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Sriwatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 149; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-x23709.
CC Compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||||
Db 1 cgcgtgcgacctctg 17

RESULT 4

AAHX18693
ID AAHX18693 standard; DNA; 17 BP.

AC AAHX18693;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #25.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;
KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW HIV; inflammation; ss.

OS Synthetic.

PN W09901579-A1.

PD 14-JAN-1999.

PF 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

PA (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

DR WPI; 1999-106077/09.

PT Composition comprising nucleic acid and penetration enhancer - used
PT particularly for delivering therapeutic antisense oligonucleotides
PT across the gastrointestinal mucosa, provides high bioavailability

PS Example 2; Page 84; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35,%. The penetration enhancer improves: (1) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAHX18693 to AAHX18799 and AAHX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||||
Db 1 cgcgtgcgacctctg 17

RESULT 5

AAH48722
ID AAH48722 standard; DNA; 20 BP.

AC AAH48722;

DT 19-OCT-2001 (first entry)

DE Proto-oncogene bcl-2 associated primer SEQ ID 3.

XX Primer; phosphorothioate; somatostatin; cytosolic; virucide; asthma;

KW antiinflammatory; antitumor; cardiatic; antisense therapy;
KW cancer; viral disease; inflammatory process; somatostatin receptor;
KW central nervous system disease; cardiovascular disease; SSTR;

KW proto-oncogene; bcl-2; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified_base 1..20
FT /tag= a
FT /mod_base= "OTHER"
FT /note= "phosphorothioate"

PN DE10006572-A1.

PD 23-AUG-2001.

PF 14-FEB-2000; 2000DE-1006572.

PR 14-FEB-2000; 2000DE-1006572.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Eisenhut M, Mier W, Ertla R, Haberkorn U;

DR WPI; 2001-530596/59.

PT New conjugates of oligonucleotides with somatostatin analogs, useful in
PT antisense therapy, e.g. of viral, inflammatory or asthmatic disease or
PT especially tumors overexpressing the somatostatin receptor -

PS Example 3; Page 9; 16pp; German.

XX This invention describes a novel oligonucleotide conjugate (I) comprising
CC (a) an oligonucleotide, at least part of the sequence of which is
CC complementary to part of an intracellular nucleic acid sequence; and (b)
CC a somatostatin analog. The products of the invention have cytostatic,
CC virucide, antiinflammatory, antitumor and cardiatic activity. The use
CC of (I) is claimed in antisense therapy, especially of cancer, viral
CC disease, inflammatory processes or asthmatic, central nervous system or
CC cardiovascular disease. (I) are especially used for therapy of tumors
CC overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung
CC tumors, breast tumors, brain tumors or other endocrine tumors), but are
CC also useful for treating viral diseases (e.g. herpes simplex-1
CC infection), inflammatory disease (typical target RNA the NF-Kappa-B),
CC asthmatic disease (typical target RNA the adenosine A1 receptor), central
CC nervous system disease (typical target RNA the dopamine receptor) or
CC cardiovascular disease (typical target RNA c-myc). (I) are efficiently
CC taken up by cells and incorporated in target cells (via the SSTR) and are
CC highly selective for cells overexpressing SSTR's. This sequence
CC represents a primer used to illustrate the method of the invention.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 20;

Best Local Similarity 94.1%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||

Db 4 cgtgtgcgacctctg 20

RESULT 6

AAV52546 standard; DNA; 18 BP.

AAV52546;

20-NOV-1998 (first entry)

Unmethylated Cpg dinucleotide 1761.

Unmethylated Cpg dinucleotide; immune response; bacterial meningitis;
natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
pulmonary disorder; asthma; environmentally induced airway disease;
bacterial infection; endotoxaemia; therapy; cystic fibrosis;
inflammatory bowel disease; ss.

Synthetic.

WO9837919-A1.

03-SEP-1998.

25-FEB-1998; 98WO-US03678.

28-FEB-1997; 97US-0039405.

(IOWA) UNIV IOWA RES FOUND.

Krieg AM, Schwartz DA;

WPI; 1998-480941/41.

Use of nucleic acids containing an unmethylated Cpg - for treating a
subject having or at risk of having an acute decrement in air flow
or inhibiting an inflammatory response

Example 4; Page 35; 65pp; English.

This sequence represents an unmethylated Cpg dinucleotide, and can be
used in the method of the invention. The method is for treating a subject
having, or at risk of having an acute decrement in air flow, comprising
administering a nucleic acid sequence containing at least one
unmethylated Cpg. The nucleic acid contains an unmethylated Cpg
dinucleotide affect an immune response in a subject by activating natural
killer cells (NK) or redirecting a subject's immune response from a Th2
to a Th1 response by inducing monocytic and other cells to produce Th1
cytokines. They can be used to treat pulmonary disorders having an
immunologic component, such as asthma or environmentally induced airway
disease. They can also be used to treat diseases associated with
Gram-positive bacterial infections or endotoxaemia including bacterial
meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
abscess, haemorrhagic shock, disseminated intravascular coagulation, or
an inflammatory response to lipopolysaccharide.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctct 15

|||||

4 cgcgtgcgacctct 18

RESULT 7

AAV27720 standard; DNA; 18 BP.

AAV27720;

01-OCT-1998 (first entry)

Immunostimulatory oligodeoxynucleotide of the invention.

Immunostimulatory; oligodeoxynucleotide; ODN;
unmethylated Cpg dinucleotide; activate; lymphocyte; immune response;
Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
desensitisation therapy; artificial adjuvant; antibody generation; ss.

Synthetic.

WO9818810-A1.

07-MAY-1998.

30-OCT-1997; 97WO-US19791.

30-OCT-1996; 96US-0738652.

(IOWA) UNIV IOWA RES FOUND.

Krieg AM;

WPI; 1998-272127/24.

New immunostimulatory nucleic acid molecules - which contain at
least one unmethylated Cpg dinucleotide, used for treating e.g.
tumours, infections or autoimmune disease

Disclosure; Page 49; 109pp; English.

AAV27641-751 represent immunostimulatory oligodeoxynucleotides
(ODNs) of the invention. The ODNs contain at least one unmethylated Cpg
dinucleotide, and have the formula:
5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
Cpgs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N
is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and
N2 does not contain a CCGG tetramer or more than one CCG or CCG trimer
OR 5' NX1X2CGX3X4N 3', where at least one nucleotide separates
consecutive Cpgs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA,
X3 and X4 are selected from TpT or CpT, N is any nucleotide and N1+N2 is
0-26 bases with the provision that N1 and N2 does not contain a CCGG
tetramer or more than one CCG or CCG trimer.
The ODNs activate lymphocytes in a subject and redirect a subject's
immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells
and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
autoimmune diseases, in desensitisation therapy, as an artificial
adjuvant during antibody generation in a mammal such as a mouse or a
human.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctct 15

|||||

4 cgcgtgcgacctct 18

RESULT 8

AAZ41906 standard; DNA; 18 BP.

AAZ41906;

24-JAN-2000 (first entry)

XX IL-12 secretion inducing Cpg oligonucleotide 51.
DE Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
XX human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW antigen presenting cell; infection; allergic disease.
XX Synthetic.
XX WO951259-A2.
PN 14-OCT-1999.
XX 02-APR-1999; 99WO-US07335.
XX 03-APR-1998; 98US-0080729.
XX (IOWA) UNIV IOWA RES FOUND.
XX Krieg AM, Weiner G;
PI MPI; 1999-620169/53.
XX Novel synergistic combinations of immunostimulatory oligonucleotides
PT and immunopotentiating cytokines are useful for stimulating the immune
PT system -
XX Example 8; Page 80; 91pp; English.
XX Sequences AA241856-241949 are phosphorothioate Cpg oligonucleotides
XX which are used in the invention to induce interleukin-12 (IL-12)
CC secretion from human PBMC. The invention comprises stimulating an immune
CC response in a subject comprising administering to a subject exposed to an
CC antigen, an immunopotentiating cytokine and an immunostimulatory Cpg
CC oligonucleotide to induce a synergistic antigen specific immune
CC response. The methods are useful for treating cancer by stimulating an
CC antigen specific immune response against a cancer antigen. The methods
CC can also be used to treat neoplastic disorders in humans, including but
CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC for treating infectious diseases, e.g. viral diseases such as HIV,
CC bacterial diseases, and fungal diseases. The methods may also be used to
CC treat allergic diseases, e.g. asthma. The methods and compositions may
CC also be applied to treat cancer and tumours in non human subjects,
CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC be treated and include leukæmia, haemangioepithelioma and bovine ocular
CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC caused by the bacterium *Corynebacterium pseudotuberculosis*, and
CC contagious lung tumour of sheep caused by *jaagsiekte* may also be
CC treated. Cpg oligonucleotides can be useful in activating B cells, NK
CC cells, and antigen presenting cells, such as monocytes and macrophages.
CC Cpg oligonucleotides enhance antibody dependent cellular cytotoxicity and
CC can be used as an adjuvant in conjunction with tumour antigens to
CC protect against a tumour challenge.
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 88.2%; Score 15; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgaccctct 15
|||||
DB 4 cgcgtgcgaccctct 18

RESULT 9
AA247644 standard; DNA; 18 BP.
ID AA247644
XX
AC AA247644;

XX 01-MAR-2000 (first entry)
DE Parasitic infection preventing exemplary oligonucleotide SEQ ID NO:50.
XX Immune system; immunostimulatory; parasitic infection; parasite;
KW Cpg oligonucleotide; antigen presenting cell; natural killer cell;
KW granulocyte; malaria; helminth disease; tick; mite; ss.
XX Synthetic.
XX WO956755-A1.
PN 11-NOV-1999.
XX 06-MAY-1999; 99WO-US09863.
XX 06-MAY-1998; 98US-0084512.
XX (IOWA) UNIV IOWA RES FOUND.
XX (OTTA-) OTTAWA CIVIC LOEB RES INST.
XX (USNA) US SEC OF NAVY.
XX Gramzinski RA, Krieg AM, Davis HL, Hoffman SL;
PI MPI; 2000-062123/05.
XX Treating and preventing parasitic infections using Cpg oligonucleotides
PT disclosure; Page 20; 74pp; English.
XX The present invention describes a method for treating and preventing
XX parasitic infection by administration of unmethylated Cpg
XX oligonucleotides. The Cpg oligonucleotides are able to stimulate the
XX innate immune system via the activation of immune cells, such as antigen
XX presenting cells, natural killer cells and granulocytes. The Cpg
XX oligonucleotides and the method can be used to treat and prevent
XX parasitic diseases, such as malaria, helminth diseases, tick and mites
XX in humans, animals and poultry. The oligonucleotides may be administered
XX in conjunction with parasitocides or other therapeutic compounds after
XX an organism has been diagnosed to be infected with parasites. Diseases
XX which can be treated or prevented include those caused by *Plasmodium*
XX *falciparum*, *P. ovale*, *P. malariae*, *P. vivax*, *P. knowlesi*, *Babesia*
XX *microti*, *B. divergens*, *Trypanosoma cruzi*, *T. gambiense*, *T. rhodesiense*,
XX *Schistosoma mansoni*, *Toxoplasma gondii*, *Trichinella spiralis*, *Leishmania*
XX *major*, *L. donovani*, *L. braziliensis*, and *L. tropica*. The parasite is
XX especially capable of causing malaria. The present sequence represents
XX a parasitic infection preventing exemplary oligonucleotide sequence from
XX the present invention.
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
QY 1 cgcgtgcgaccctct 15
|||||
DB 4 cgcgtgcgaccctct 18

RESULT 10
AA247982 standard; DNA; 18 BP.
ID AA247982
XX
AC AA247982;
XX
XX 08-MAR-2000 (first entry)
DE Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.
XX Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;
KW

KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
KW immune response; allergic reaction; infectious disease; asthma;
KW thrombocytopaenia; immunohaemolytic disorder; genetic disorder;
KW hemoglobinopathy; kidney failure; chronic inflammatory disorder;
KW rheumatoid arthritis; ss.

OS Synthetic.

PN WO9558118-A2.

PD 18-NOV-1999.

PF 14-MAY-1999; 99WO-IB01285.

PR 14-MAY-1998; 98US-0085516.

PR 02-FEB-1999; 99US-0241653.

PA (CPGT-) CPG IMMUNOPHARMACEUTICALS GMBH.

PA (CPGT-) CPG IMMUNOPHARMACEUTICALS INC.

PI Wagner H, Lipford G;

DR WPI; 2000-062261/05.

PT Use of CPG containing oligonucleotides for, e.g. inducing an
PT antigen-specific immune response

PS Example 1; Page 66; 116pp; English.

CC The present invention describes a method using CPG containing
CC oligonucleotides (ONS) for regulating immune system remodeling and for
CC regulating haematopoiesis. The method for inducing an antigen-specific
CC immune response comprises: (1) administering an ON having a sequence
CC including at least the formula (1); and (2) exposing the subject to an
CC antigen at least 3 days after the ON is administered to the subject to
CC produce an antigen-specific immune response: 5' X1CGX2 3' (1), where
CC the ON = includes at least 8 nucleotides; C and G = unmethylated, and
CC X1 and X2 = nucleotides. The method can be used for inducing an immune
CC response against an antigen such as cells, cell extracts, proteins,
CC polysaccharides, viral extracts, viruses, bacteria, fungi, parasites and
CC catholytates, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or
CC an allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia
CC which is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as
CC drug-induced anaemia, immunohaemolytic disorder, genetic disorders such
CC as haemoglobinopathy and inherited haemolytic anaemia, inadequate
CC production despite adequate iron stores, chronic disease such as kidney
CC failure, and chronic inflammatory disorder such as rheumatoid arthritis,
CC or anaemia resulting from accidental or therapeutic radiation exposure.
CC AA47932 to AA48029 represent phosphorothioate CPG oligonucleotides
CC used in the exemplification of the present invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 21; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgcgtgcgacctct 15
| | | | | | | | | | | | | | | | | |
Db 4 cgcgtgcgacctct 18

RESULT 11

AAH50628

ID AAH50628 standard; DNA; 18 BP.

AC AAH50628;

XX

DT 22-AUG-2001 (first entry)

XX Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.

DE Immunostimulatory; inducing; natural killer cell; lytic activity;

KW unmethylated CPG dinucleotide; immune response; B cell proliferation;

KW Th1; immune activation; interleukin 6; IL-6; interferon gamma;

KW IFN-gamma; cytokine; ss.

XX Homo sapiens.

OS Synthetic.

PN US6239116-B1.

PD 29-MAY-2001.

PF 30-OCT-1997; 97US-0960774.

PR 30-OCT-1996; 96US-0738652.

PA (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GROUP INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Krieger AM, Kline JN;

DR WPI; 2001-380456/40.

PT Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
PT natural killer cell lytic activity in a human, comprise administering
PT to the subject or exposing a natural killer cell to immunostimulatory
PT nucleic acids

PS Disclosure; Column 32; 74pp; English.

CC The present invention describes methods for inducing interleukin 6
CC (IL-6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating
CC natural killer cell lytic activity. The methods comprise administering
CC to the subject or exposing a natural killer cell to an immunostimulatory
CC nucleic acid. Also described are: (1) inducing IL-6 in a subject
CC comprising administering to the subject to induce IL-6 in a subject
CC the immunostimulatory nucleic acid; (2) stimulating natural killer cell
CC lytic activity comprising exposing a natural killer cell to the
CC immunostimulatory nucleic acid to stimulate natural killer cell
CC activity; (3) inducing interferon-gamma in a subject to treat an immune
CC system deficiency comprising administering to the subject to induce
CC interferon-gamma production, the immunostimulatory nucleic acid; and
CC (4) inducing IL-12 in a subject comprising administering to the subject
CC IL-6, interferon-gamma or IL-12, or stimulating natural killer cell
CC lytic activity in a subject, particularly a human. The methods are
CC particularly useful for modulating an immune response. AAH50571 to
CC AAH50671 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgcgtgcgacctct 15
| | | | | | | | | | | | | | | | | |
Db 4 cgcgtgcgacctct 18

RESULT 12

AAf98888

ID AAf98888 standard; DNA; 18 BP.

XX

AC AAf98888;

XX

DT 12-JUN-2001 (first entry)
XX Immunostimulatory nucleic acid #4.
DE
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000MO-US26383.
PF
XX
XX 25-SEP-1999; 99US-0156113.
PR
XX 27-SEP-1999; 99US-0156135.
PR
XX 23-AUG-2000; 2000US-0227436.
XX
XX (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX Kriegl AM, Schetter C, Vollmer J;
PI
XX
XX WPI; 2001-273485/28.
DR
XX
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
PS
XX
XX Disclosure; Page 38; 338pp; English.
PS
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (Py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
CC
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 88.2%; Score 15; DB 22; Length 18;
Best local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgcgtgcgacctct 15
| | | | | | | | | | | | | | | | | |
DB 4 cgcgtgcgacctct 18

RESULT 13
AAF98931
ID AAF98931 standard; DNA: 18 BP.
XX
AC AAF98931;
XX
XX 12-JUN-2001 (first entry)
DT
XX
XX Immunostimulatory nucleic acid #47.
DE
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;

KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000MO-US26383.
PF
XX
XX 25-SEP-1999; 99US-0156113.
PR
XX 27-SEP-1999; 99US-0156135.
PR
XX 23-AUG-2000; 2000US-0227436.
XX
XX (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX Kriegl AM, Schetter C, Vollmer J;
PI
XX
XX WPI; 2001-273485/28.
DR
XX
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
PS
XX
XX Disclosure; Page 39; 338pp; English.

CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (Py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
CC
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 88.2%; Score 15; DB 22; Length 18;
Best local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctct 15
| | | | | | | | | | | | | | | | | |
DB 4 cgcgtgcgacctct 18

RESULT 14
AAQ86651
ID AAQ86651 standard; DNA: 17 BP.
XX
AC AAQ86651;
XX
XX 27-SEP-1995 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW lymphoma; programmed cell death; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1.17
FT misc_feature
FT /*tag= a
FT /note= "3'-5' (antisense) sequence"
XX

PN W09508350-A.
 XX
 PD 30-MAR-1995.
 XX
 PF 20-SEP-1994; 94WO-US10725.
 XX
 PR 20-SEP-1993; 93US-0124256.
 XX
 PA (REED/) REED J C.
 XX
 PI Reed JC;
 XX
 DR WPI; 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Example 12; Page 33; 108pp; English.
 XX
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA08650-55) or the 5'-cap
 CC region (AA08656-58) of human bcl-2 pre-mRNAs. The AA08651
 CC oligonucleotide provided pronounced DNA fragmentation.
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgaccctc 14
 |||||
 DB 4 cgcgtgcgaccctc 17

RESULT 15
 AAT67093/C
 ID AAT67093 standard; DNA: 45 BP.
 XX
 AC AAT67093;
 XX
 DT 08-AUG-1997 (first entry)
 XX
 DE K-ATP channel subunit Kir6.2 3'UTR probe.
 XX
 KW ATP-sensitive potassium ion channel; K-ATP channel; Kir6.2;
 KW probe; ss.
 XX
 OS Synthetic.
 XX
 PN W09718308-A2.
 XX
 PD 22-MAY-1997.
 XX
 PF 18-NOV-1996; 96WO-GB02831.
 XX
 PR 16-NOV-1995; 95GB-0023497.
 XX
 PA (WELL) WELLCOME TRUST LTD.
 XX
 PI Ashcroft F, Ashcroft SJH, Ashfield R, Sakura H;
 XX
 DR WPI; 1997-289284/26.
 XX
 PT Kir6.2 gene encoding protein that forms ATP-sensitive potassium ion
 PT channel - useful to treat disease associated with abnormal coupling
 PT of cellular metabolism to potassium fluxes and/or electrical
 PT activity
 XX
 PS Example 7; Page 34; 61pp; English.

XX A DNA probe (AAT67093) is based on the 3' untranslated region of the
 CC mouse K-ATP channel Kir6.2 gene (see also AAT67087), starting at
 CC nucleotide +85. Probes (AAT67092-95) based on Kir6.2 and SUR1
 CC sequences were used for in-situ hybridisation analysis of samples
 CC from adult rat and mouse brain sections. The probes were designed
 CC for least similarity to other subfamily members to minimise
 CC cross-hybridisation. The results indicated the the brain K-ATP
 CC channel has Kir6.2 (see also AAW17931-32) and SUR1 subunits.
 XX
 SQ Sequence 45 BP; 11 A; 18 C; 7 G; 9 T; 0 other;

Query Match 75.3%; Score 12.8; DB 18; Length 45;
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gcttcgaccctctg 17
 |||||
 DB 23 GGTTCGAGCCTCTTG 8

Search completed: June 28, 2002, 22:40:12
 Job time: 8088 sec

Mon Jul 1 08:41:00 2002

us-09-709-170a-8.szlm75.rng

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run On: June 28, 2002, 22:16:45 ; Search time 334.55 Seconds
(Without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-8

Perfect score: 17

Sequence: 1 cgcgtgcagacctctg 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17	100.0	2	US-08-465-485A-8
2	17	100.0	3	US-09-080-285-8
3	15	88.2	18	US-09-030-701-28
4	15	88.2	18	US-09-286-098-60
5	15	88.2	18	US-08-960-774-60
6	14	82.4	17	US-08-465-485A-9
7	14	82.4	17	US-09-080-285-9
8	12.2	71.8	31	US-08-095-726-25
9	12.2	71.8	31	US-08-095-726-27
10	12.2	71.8	31	US-08-096-043-22
11	12.2	71.8	31	US-08-096-043-24
12	12.2	71.8	31	US-08-093-577-18
13	12.2	71.8	31	US-08-093-577-20
14	12.2	71.8	31	US-08-096-623A-30
15	12.2	71.8	31	US-08-096-623A-32
16	12.2	69.4	18	US-09-205-143-51
17	11.8	67.1	30	US-08-809-185-3
18	11.4	67.1	34	US-08-809-185-5
19	11.4	65.9	21	US-08-357-146-7
20	11.2	65.9	21	US-09-154-344-7
21	11.2	65.9	33	US-08-873-479-39
22	11.2	65.9	35	US-08-959-212-11
23	11.2	65.9	37	US-09-031-442A-7
24	11.2	65.9	37	US-09-258-377-7
25	11.2	65.9	50	US-08-137-117D-60
26	11.2	65.9	50	US-08-436-717-60
27	11.2	65.9	50	US-08-974-631-13

C	28	11.2	65.9	71	4	US-09-025-769B-95	Sequence 95, Appl
	29	11	64.7	17	3	US-08-465-485A-10	Sequence 10, Appl
	30	11	64.7	17	3	US-09-080-285-10	Sequence 10, Appl
	31	11	64.7	17	4	US-08-584-040-7553	Sequence 7553, Ap
C	32	11	64.7	67	4	US-09-025-769B-83	Sequence 83, Appl
	33	10.8	63.5	21	4	US-08-943-731-266	Sequence 266, Ap
	34	10.8	63.5	24	2	US-08-859-998-1250	Sequence 1250, Ap
	35	10.8	63.5	24	4	US-08-859-998-1250	Sequence 1250, Ap
	36	10.8	63.5	33	3	US-08-461-030C-5	Sequence 5, Appl
	37	10.8	63.5	33	3	US-08-744-138-12	Sequence 12, Appl
	38	10.8	63.5	33	4	US-09-241-376-12	Sequence 12, Appl
	39	10.8	63.5	33	5	PCT-US95-07135-5	Sequence 5, Appl
	40	10.8	63.5	49	1	US-08-171-389-43	Sequence 43, Appl
	41	10.8	63.5	49	1	US-08-123-936-43	Sequence 43, Appl
	42	10.8	63.5	49	2	US-08-475-228A-43	Sequence 43, Appl
	43	10.8	63.5	49	3	US-08-482-080A-43	Sequence 43, Appl
	44	10.8	63.5	49	5	PCT-US93-12388-43	Sequence 43, Appl
C	45	10.8	63.5	54	1	US-08-373-124A-2236	Sequence 2236, Ap

ALIGNMENTS

RESULT 1
US-08-465-485A-8
Sequence 8, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-8

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctcttg 17
|||||
Db 1 cgcgtgcgacctcttg 17

RESULT 2

US-09-080-285-8
; Sequence 8, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-8

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctcttg 17
|||||
Db 1 cgcgtgcgacctcttg 17

RESULT 3
US-09-030-701-28
; Sequence 28, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; FILE REFERENCE: C1039/77011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; US-09-030-701-28

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctt 15
|||||
Db 4 cgcgtgcgacctctt 18

RESULT 4
US-09-286-098-60
; Sequence 60, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-286-098-60

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctt 15
|||||
Db 4 cgcgtgcgacctctt 18

RESULT 5

US-08-960-774-60
; Sequence 60, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieger et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-960-774-60

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctc 15
|||||
DB 4 CGCGTGCACCTCT 18

RESULT 6
US-08-465-485A-9
; Sequence 9, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; CLASSIFICATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctc 14
|||||
DB 4 CGCGTGCACCTCT 17

RESULT 7
US-09-080-285-9
; Sequence 9, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcacccctc 14
||| ||||| |||||
DB 4 CGCGTCGCACCCCTC 17

RESULT 8

US-08-095-726-25
Sequence 25, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis In
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128564972
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-25

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcacccctc 17
||| ||||| |||||
DB 4 CGCGTCGCACCCCTGTG 20

RESULT 9

US-08-095-726-27/c
Sequence 27, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis In
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128564972
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-27

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcacccctc 17
||| ||||| |||||
DB 28 CGCGTCGCACCCCTGTG 12

RESULT 10
US-08-096-043-22
Sequence 22, Application US/08096043
Patent No. 5530189
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Profitit, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Lycopen Biosynthesis in
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-043-22

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgcgtcgaccctctg 17
||| ||||| |||
Db 4 CGCATCGACCCCTGTG 20

RESULT 11
US-08-096-043-24/c
Sequence 24, Application US/08096043
Patent No. 5530189
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Profitit, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Lycopen Biosynthesis in
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept

STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-043-24

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgcgtcgaccctctg 17
||| ||||| |||
Db 28 CGCATCGACCCCTGTG 12

RESULT 12
US-08-093-577-18
Sequence 18, Application US/08093577
Patent No. 5545816
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Profitit, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Phytoene Biosynthesis in
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,577
FILING DATE: 19-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,569

FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-093-577-18

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
||| ||||| ||
Db 4 CGCATGCGACCTTGTC 20

RESULT 13
US-08-093-577-20/c
Sequence 20, Application US/08093577
Patent No. 5545816
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Phytoene Biosynthesis in
NUMBER OF SEQUENCES: 43
TITLE OF INVENTION: Genetically Engineered Hosts
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,577
FILING DATE: 19-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-093-577-20

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
||| ||||| ||
Db 28 CGCATGCGACCTTGTC 12

RESULT 14
US-08-096-623A-30
Sequence 30, Application US/08096623A
Patent No. 5684238
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of zeaxanthin and
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-623A-30

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgcgcgcacctcttg 17
||| ||||| ||
Db 4 CGCATGCGACCTTGTG 20

RESULT 15

US-08-096-623A-32/c
; Sequence 32, Application US/08096623A
; Patent No. 5684238

GENERAL INFORMATION:

APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Profit, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of zeaxanthin and
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: AMO-006.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 655-1500
TELEFAX: (312) 655-1501

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-096-623A-32

QY 1 cgcgtgcgcacctcttg 17
||| ||||| ||
Db 28 CGCATGCGACCTTGTG 12

Search completed: June 28, 2002, 22:16:46
Job time: 8272 sec

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Mon Jul 1 08:41:00 2002

us-09-709-170a-8.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:05 ; Search time 3762.88 Seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-9

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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17: em_hum: *
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19: em_mu: *
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25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description
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1	17	100.0	17	6	AR052611	AR052611 Sequence
2	17	100.0	18	6	AR146348	AR146348 Sequence
3	17	100.0	18	6	AR154731	AR154731 Sequence
4	17	100.0	18	6	AX103812	AX103812 Sequence
5	17	100.0	18	6	AX103864	AX103864 Sequence
6	17	100.0	18	6	AX355457	AX355457 Sequence
7	17	100.0	18	6	BD009122	BD009122 Sequence
8	14	82.4	17	6	AR052610	AR052610 Sequence
9	14	82.4	17	6	AR052612	AR052612 Sequence
10	13.8	81.2	24	6	BD010808	BD010808 Sequence
11	12.8	75.3	51	6	AX162817	AX162817 Sequence
12	12.8	75.3	51	6	AX162819	AX162819 Sequence
13	12.8	75.3	51	6	E12821	E12821 Sequence
14	11.8	69.4	18	6	E12821	E12821 Sequence
15	11.8	69.4	18	6	E21868	E21868 Sequence
16	11.8	69.4	18	6	E21869	E21869 Sequence
17	11.8	69.4	20	6	AX296262	AX296262 Sequence
18	11.8	69.4	24	6	AX291629	AX291629 Sequence
19	11.4	67.1	31	6	AX179386	AX179386 Sequence
20	11.4	67.1	31	6	I24847	I24847 Sequence
21	11.4	67.1	31	6	I24849	I24849 Sequence
22	11.4	67.1	31	6	I72670	I72670 Sequence
23	11.4	67.1	31	6	I72670	I72670 Sequence
24	11.4	67.1	33	6	AX14926	AX14926 Sequence
25	11.4	67.1	51	6	AX164886	AX164886 Sequence
26	11.2	65.9	19	6	AR152817	AR152817 Sequence
27	11.2	65.9	28	6	AR003376	AR003376 Sequence
28	11.2	65.9	28	6	I21165	I21165 Sequence
29	11.2	65.9	28	6	I74432	I74432 Sequence
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33	11.2	65.9	39	6	AX162310	AX162310 Sequence
34	11.2	65.9	44	6	I32830	I32830 Sequence
35	11.2	65.9	49	6	AX279745	AX279745 Sequence
36	11.2	65.9	51	6	AX158282	AX158282 Sequence
37	11.2	65.9	51	6	AX162808	AX162808 Sequence
38	11.2	65.9	51	6	AX162818	AX162818 Sequence
39	11.2	65.9	55	6	AX162820	AX162820 Sequence
40	11.2	65.9	55	6	AR101983	AR101983 Sequence
41	11.2	65.9	59	6	I32832	I32832 Sequence
42	11.2	65.9	59	12	SYNECOCVK	SYNECOCVK Sequence
43	11.2	65.9	69	6	AR101981	AR101981 Sequence
44	11.2	65.9	17	6	AR052613	AR052613 Sequence
45	11	64.7	67	6	A60774	A60774 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR052611 17 bp DNA
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES
SOURCE Location/Qualifiers
BASP COUNT: 2 a 8 c 4 g 3 t
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Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
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Db 1 TACCGGTGAGACCCTC 17

RESULT 2
ARI46348 18 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 60 from patent US 6218371.
DEFINITION ARI46348
ACCESSION ARI46348
VERSION ARI46348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines
JOURNAL Patent: US 6218371-A 60 17-APR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
ARI54731 18 bp DNA linear PAT 08-AUG-2001
LOCUS ARI54731
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION ARI54731
VERSION ARI54731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
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Db 1 TACCGGTGAGACCCTC 17

RESULT 4
AX103812 18 bp DNA linear PAT 30-APR-2001
LOCUS AX103812
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812

VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TACCGGTGAGACCCTC 17

RESULT 5
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LOCUS AX103864
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TACCGGTGAGACCCTC 17

RESULT 6
AX355457 18 bp DNA linear PAT 06-FEB-2002
LOCUS AX355457
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.

TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"
BASE COUNT 2 a 8 c 4 g 4 t
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Query Match 100.0%; Score 17; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TACCGCTGCGACCCCTC 17

RESULT 7
BD009122 18 bp DNA linear PAT 31-JAN-2002
LOCUS Immunostimulatory nucleic acid molecules.
DEFINITION BD009122.1 GI:18637495
VERSION JP 2001503267-A/74.
KEYWORDS JP 2001503267-A/74.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl, A.M. and Kline, J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PF 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEGL, JOEL N KLINE
PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,
PC A61K31/70
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FH Key Location/Qualifiers
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/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgacccctc 17
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Db 1 TACCGCTGCGACCCCTC 17

RESULT 8
AR052610 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 8 from patent US 5831066.
DEFINITION AR052610
ACCESSION AR052610
VERSION AR052610.1 GI:5975974

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 8 03-NOV-1998;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgacccctc 17
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Db 1 CGCGTGGACCCCTC 14

RESULT 9
AR052612 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 10 from patent US 5831066.
DEFINITION AR052612
ACCESSION AR052612.1 GI:5975976
VERSION AR052612.1 GI:5975976
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 10 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgaccc 14
|||||
Db 4 TACCGCTGCGACCC 17

RESULT 10
BD010808 24 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
DEFINITION BD010808
ACCESSION BD010808.1 GI:18639181
VERSION JP 2001069994-A/9.
KEYWORDS JP 2001069994-A/9.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911
PR
PI YASUNAKI ITO, KAZUMORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 2 TACGCGTGCGCCCATC 18

RESULT 11
AXI62807
LOCUS AXI62807 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6135 from Patent WO0140521.
ACCESSION AXI62807
VERSION AXI62807.1 GI:14544138
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6135 07-JUN-2001;
Curagen Corporation (US)
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source Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 15 ACCGCGTGCGCCCATC 30

RESULT 12
AXI62817
LOCUS AXI62817 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6145 from Patent WO0140521.
ACCESSION AXI62817

VERSION AXI62817.1 GI:14544148
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6145 07-JUN-2001;
Curagen Corporation (US)
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgaccctc 17
DB 18 ACCGCGTGCGCCCATC 33

RESULT 13
AXI62819
LOCUS AXI62819 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6147 from Patent WO0140521.
ACCESSION AXI62819
VERSION AXI62819.1 GI:14544150
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6147 07-JUN-2001;
Curagen Corporation (US)
FEATURES
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misc_feature 26
/note='1 of 2 allelic variants (6148 is other entry)
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Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgaccctc 17
DB 18 ACCGCGTGCGCCCATC 33

RESULT 14
AXI62921
LOCUS AXI62921 18 bp DNA linear PAT 24-JUN-1998
DEFINITION Antisense oligonucleotide against WT1 mRNA.

ACCESSION E12921
VERSION E12921.1 GI:3251752
KEYWORDS JP 1997104629-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamagami,T., Inoue,K. and Sugiyama,H.
TITLE LEUKEMIA CELL PROLIFERATION INHIBITING AGENT CONTAINING ANTISENSE
JOURNAL OLIGONUCLEOTIDE DERIVATIVE AGAINST WILMS TUMOR GENE (WT1)
KISHIMOTO CHUZO, SUGIYAMA HARUO
COMMENT OS None
OC Artificial sequences.
PN JP 1997104629-A/1
PD 22-APR-1997
PF 16-MAY-1996 JP 1996144818
PR 01-JUN-1995 JP 95P 156672
PI YAMAGAMI TAMOTSU, INOUE KAZUJI, SUGIYAMA HARUO PC
A61K31/70,A61K48/00,C07H21/04;
CC strandedness: Single;
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DB 15 ACCGCATTCGACCT 1

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LOCUS E21868
DEFINITION Solid tumor remedy comprising expression inhibitor against Wilms
tumor (WT1).
ACCESSION E21868
VERSION E21868.1 GI:13023739
KEYWORDS JP 1999035484-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Haruo,S.
TITLE Solid tumor remedy comprising expression inhibitor against Wilms
tumor (WT1)
JOURNAL Patent: JP 1999035484-A 1 09-FEB-1999;
HARUO SUGIYAMA
COMMENT OS Unidentified
PN JP 1999035484-A/1
PD 09-FEB-1999
PF 16-JUL-1997 JP 1997191635
PR
PI HARUO SUGIYAMA
PC A61K45/00,A61K31/70,A61K38/00,A61K48/00
CC Strandedness: Single;
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Best Local Similarity 86.7%; Pred. No. 3.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accgcgtgcgacct 16
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Search completed: June 28, 2002, 22:11:06
Job time: 8357 sec

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:12 ; Search time 1381.16 Seconds

(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170A-9

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Total number of hits satisfying chosen parameters: 1996432

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Post-processing: Minimum Match 0%

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4:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1963.DAT.*
5:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1964.DAT.*
6:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1965.DAT.*
7:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1966.DAT.*
8:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1967.DAT.*
9:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1968.DAT.*
10:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1969.DAT.*
11:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1970.DAT.*
12:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1971.DAT.*
13:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1972.DAT.*
14:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1973.DAT.*
15:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1974.DAT.*
16:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1975.DAT.*
17:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1976.DAT.*
18:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1977.DAT.*
19:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1978.DAT.*
20:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1979.DAT.*
21:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2000.DAT.*
22:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2001A.DAT.*
23:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2001B.DAT.*
24:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
No.					
1	17	100.0	17	AA086651	Bcl-2 antisense c
2	17	100.0	18	AAVS2546	UnmethyIated Cpg
3	17	100.0	18	AA217720	Immunostimulatory
4	17	100.0	18	AA41906	IL-12 secretion i
5	17	100.0	18	AA247644	Parasitic infectio
6	17	100.0	18	AA247982	Immune remodeling
7	17	100.0	18	AAHS0628	Natural killer ce
8	17	100.0	18	AAE98888	Immunostimulatory
9	17	100.0	18	AAE98931	Immunostimulatory

C	45	11.8	65.4	71	21	AAC35094
C	44	11.8	65.4	54	14	AAQ48043
C	43	11.8	65.4	54	14	AAQ47265
C	42	11.8	65.4	51	22	AAQ33119
C	41	11.8	65.4	45	12	AAQ38042
C	40	11.8	65.4	24	24	AB189179
C	39	11.8	65.4	24	24	AB189178
C	38	11.8	65.4	20	24	AB196304
C	37	11.8	65.4	18	20	AAK15833
C	36	11.8	65.4	18	20	AAK15834
C	35	11.8	65.4	18	18	AAQ45127
C	34	12.2	71.8	54	14	AAQ47266
C	33	12.2	71.8	36	22	AAK46089
C	32	12.2	71.8	29	13	AAQ33863
C	31	12.8	75.3	51	22	AA179206
C	30	12.8	75.3	51	22	AA179204
C	29	12.8	75.3	51	22	AA179194
C	28	13	76.5	20	21	AAZ49438
C	27	13	76.5	20	20	AAK18690
C	26	13	76.5	20	19	AAV28169
C	25	13	76.5	20	19	AAV28168
C	24	13	76.5	20	16	AAQ86643
C	23	13.8	81.2	24	22	AAF55071
C	22	13.8	81.2	18	22	AAH27725
C	21	14	82.4	17	20	AAK18694
C	20	14	82.4	17	20	AAK18695
C	19	14	82.4	17	20	AAK18693
C	18	14	82.4	17	20	AAK23685
C	17	14	82.4	17	20	AAK23686
C	16	14	82.4	17	20	AAK23684
C	15	14	82.4	17	19	AAV28174
C	14	14	82.4	17	19	AAV28173
C	13	14	82.4	17	19	AAV28172
C	12	14	82.4	17	16	AAQ86650
C	11	14	82.4	17	16	AAQ86652
C	10	15.4	90.6	20	22	AAH48722
C	9	15.4	90.6	20	22	AAH48722

ALIGNMENTS

RESULT 1

ID	AAQ86651	standard; DNA; 17 BP.
1	1	1

AC AAQ86651;

DT 27-SEP-1995 (first entry)
yy

DE Bcl-2 antisense oligonucleotide. xy

KW Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy
 KW Lymphoma; programmed cell death; ss.

OS Synthetic.

FH	Key	Location/Qualifiers
EE	1000 footings	1 17

/note= "3'-5' (antisense) sequence"

PN WO9508350-A

PD 30-MAR-1995
yy

PE 20-SEP-1994; 94WO-US10725

PR 20-SEP-1993; 9305-0124256; XX

PA (REED/) REED J C.
YY

Pl Reed JC;
yy

DR WPI; 1995-139394/18.
 XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Example 12; Page 33; 108bp; English.
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA08650-55) or the 5'-cap
 CC region (AA08656-58) of human bcl-2 pre-mRNAs. The AA08651
 CC oligonucleotide provided pronounced DNA fragmentation.
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;
 Query Match 100.0%; Score 17; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 taccgcgtgcgaccctc 17
 Db 1 taccgcgtgcgaccctc 17
 RESULT 2
 AAV52546
 ID AAV52546 standard; DNA; 18 BP.
 XX
 AC AAV52546;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Unmethylated CpG dinucleotide 1761.
 XX
 KM Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KM natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KM pulmonary disorder; asthma; environmentally induced airway disease;
 KM bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KM inflammatory bowel disease; ss.
 XX
 OS Synthetic.
 XX
 PN WO9837919-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 25-FEB-1998; 98WO-US03678.
 XX
 PR 28-FEB-1997; 97US-0039405.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Krieg AM, Schwartz DA;
 XX
 DR WPI; 1998-480941/41.
 XX
 PT Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow
 PT or inhibiting an inflammatory response
 XX
 PS Example 4; Page 35; 65pp; English.
 XX
 CC This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an

CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with
 CC Gram-positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 Query Match 100.0%; Score 17; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 taccgcgtgcgaccctc 17
 Db 1 taccgcgtgcgaccctc 17
 RESULT 3
 AAV27720
 ID AAV27720 standard; DNA; 18 BP.
 XX
 AC AAV27720;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Immunostimulatory oligodeoxyribonucleotide of the invention.
 XX
 KM Immunostimulatory; oligodeoxyribonucleotide; ODN;
 KM unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
 KM Th2; cytokine; treatment; prevention; asthma; autoimmune disease;
 KM desensitisation therapy; artificial adjuvant; antibody generation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9818810-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 30-OCT-1997; 97WO-US19791.
 XX
 PR 30-OCT-1996; 96US-0738652.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Kline JN, Krieg AM;
 XX
 DR WPI; 1998-272127/24.
 XX
 PT New immunostimulatory nucleic acid molecules - which contain at
 PT least one unmethylated CpG dinucleotide, used for treating e.g.
 PT tumours, infections or autoimmune disease
 XX
 PS Disclosure; Page 49; 109pp; English.
 XX
 CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides
 CC (ODNs) of the invention. The ODNs contain at least one unmethylated CpG
 CC dinucleotide, and have the formula:
 CC 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
 CC CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N
 CC is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and
 CC N2 does not contain a CCGG tetramer or more than one CCG or CCGG trimer
 CC OR 5' NX1X2CGX3X4N 3', where at least one nucleotide separates
 CC consecutive CpGs, X1 and X2 are selected from GPT, GPG, GPa, APT and APa,
 CC X3 and X4 are selected from TPT or CPT, N is any nucleotide and N1+N2 is
 CC 0-26 bases with the provision that N1 and N2 does not contain a CCGG
 CC tetramer or more than one CCG or CCGG trimer.
 CC The ODNs activate lymphocytes in a subject and redirect a subject's
 CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells
 CC and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
 CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgcacctc 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 taccgcgtgcgcacctc 17

RESULT 6

AAZ47982
ID AAZ47982 standard; DNA; 18 BP.

AAZ47982;

08-MAR-2000 (first entry)

Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.

Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;
immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
immune response; allergic reaction; infectious disease; asthma;
thrombocytopenia; immunohaemolytic disorder; genetic disorder;
haemoglobinopathy; kidney failure; chronic inflammatory disorder;
rheumatoid arthritis; ss.

Synthetic.

WO958118-A2.

18-NOV-1999.

14-MAY-1999; 99WO-IB01285.

14-MAY-1998; 98US-0085516.

02-FEB-1999; 99US-0241653.

(CPG1-) CPG IMMUNOPHARMACEUTICALS GMBH.

(CPG1-) CPG IMMUNOPHARMACEUTICALS INC.

Wagner H, Lipford G;

Use of Cpg containing oligonucleotides for, e.g. inducing an
antigen-specific immune response -

Example 1; Page 66; 116pp; English.

The present invention describes a method using Cpg containing
oligonucleotides (ONS) for regulating immune system remodeling and for
regulating haematopoiesis. The method for inducing an antigen-specific
immune response comprises: (1) administering an ON having a sequence
including at least the formula (1); and (2) exposing the subject to an
antigen at least 3 days after the ON is administered to the subject to
produce an antigen-specific immune response: 5' X1CGX2 3' (1), where
the ON = includes at least 8 nucleotides; C and G = unmethylated, and
X1 and X2 = nucleotides. The method can be used for inducing an immune
response against an antigen such as cells, cell extracts, proteins,
polysaccharides, polysaccharide conjugates, lipids, glycolipids,
carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
allergens. It can be used in a subject at risk of developing cancer or
an allergic reaction. It can also be used for treating an infectious
disease, allergic diseases and asthma, as well as thrombocytopenia
which is drug-induced, due to an autoimmune disorder such as idiopathic
thrombocytopenic purpura, or resulting from accidental or therapeutic
radiation exposure. It can also be used for treating anaemia such as
drug-induced anaemia, immunohaemolytic disorder, genetic disorders such
as haemoglobinopathy and inherited haemolytic anaemia, inadequate
production despite adequate iron stores, chronic disease such as kidney

failure, and chronic inflammatory disorder such as rheumatoid arthritis,
or anaemia resulting from accidental or therapeutic radiation exposure.
AAZ47932 to AAZ48029 represent phosphorothioate Cpg oligonucleotides
used in the exemplification of the present invention.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgcacctc 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 taccgcgtgcgcacctc 17

RESULT 7

AAH50628
ID AAH50628 standard; DNA; 18 BP.

AAH50628;

22-AUG-2001 (first entry)

Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.

Immunostimulatory; inducing; natural killer cell; lytic activity;
unmethylated Cpg dinucleotide; immune response; B cell proliferation;
TNF; immune activation; interleukin 6; IL-6; interferon gamma;
IFN-gamma; cytokine; ss.

Homo sapiens.

Synthetic.

US6239116-B1.

29-MAY-2001.

30-OCT-1997; 97US-0960774.

30-OCT-1996; 96US-0738652.

(IOWA) UNIV IOWA RES FOUND.

(COLE-) COLEY PHARM GROUP INC.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Krieg AM, Kline JN.

WPI; 2001-380456/40.

Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
natural killer cell lytic activity in a human, comprise administering
to the subject or exposing a natural killer cell to immunostimulatory
nucleic acids -

Disclosure; Column 32; 74pp; English.

The present invention describes methods for inducing interleukin 6
(IL-6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating
natural killer cell lytic activity. The methods comprise administering
to the subject or exposing a natural killer cell to an immunostimulatory
nucleic acid. Also described are: (1) inducing IL-6 in a subject
comprising administering to the subject to induce IL-6 in the subject
the immunostimulatory nucleic acid; (2) stimulating natural killer cell
lytic activity comprising exposing a natural killer cell to the
immunostimulatory nucleic acid to stimulate natural killer cell lytic
activity; (3) inducing interferon-gamma in a subject to treat an immune
system deficiency comprising administering to the subject to induce
interferon-gamma production, the immunostimulatory nucleic acid; and
(4) inducing IL-12 in a subject comprising administering to the subject
the immunostimulatory nucleic acid. The methods are useful for inducing
IL-6, interferon-gamma or IL-12, or stimulating natural killer cell

CC lytic activity in a subject, particularly a human. The methods are
CC particularly useful for modulating an immune response. AAH50571 to
CC AAH50671 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgctgcgaccctc 17
|||||

DB 1 taccgctgcgaccctc 17

RESULT 8

AAH98888 standard; DNA; 18 BP.

XX AAF98888;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #4.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

XX Immunostimulatory; tumour; viral infection; bacterial infection;

XX Fungal infection; parasitic infection; cancer; asthma;

XX Infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 98US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma

XX using immunostimulatory Py-rich and Tg nucleic acids -

XX Disclosure; Page 38; 338pp; English.

XX The present invention relates to a method for stimulating an immune

XX response. The method comprises administering an immunostimulatory nucleic

XX acid to a non-rodent subject in sufficient quantity to stimulate an

XX immune response. The present sequence is one such immunostimulatory

XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich

XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects

XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae

XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

XX haemophilus, campylobacter, clostridium, Escherichia coli and/or

XX streptococcus), fungal antigens and/or parasitic antigens. The method is

XX also useful for preventing cancer, asthma, infectious disease, allergy or

XX immune deficiency. The present sequence can also be used to redirect a

XX T_H2 to a T_H1 immune response and to activate immune cells.

XX Note: The present sequence may have a phosphorothioate backbone.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgctgcgaccctc 17
|||||

DB 1 taccgctgcgaccctc 17

RESULT 9

AAH98931 standard; DNA; 18 BP.

XX AAF98931;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #47.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

XX Immunostimulatory; tumour; viral infection; bacterial infection;

XX Fungal infection; parasitic infection; cancer; asthma;

XX Infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 98US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma

XX using immunostimulatory Py-rich and Tg nucleic acids -

XX Disclosure; Page 39; 338pp; English.

XX The present invention relates to a method for stimulating an immune

XX response. The method comprises administering an immunostimulatory nucleic

XX acid to a non-rodent subject in sufficient quantity to stimulate an

XX immune response. The present sequence is one such immunostimulatory

XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich

XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects

XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae

XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

XX haemophilus, campylobacter, clostridium, Escherichia coli and/or

XX streptococcus), fungal antigens and/or parasitic antigens. The method is

XX also useful for preventing cancer, asthma, infectious disease, allergy or

XX immune deficiency. The present sequence can also be used to redirect a

XX T_H2 to a T_H1 immune response and to activate immune cells.

XX Note: The present sequence may have a phosphorothioate backbone.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgctgcgaccctc 17
|||||

Db 1 taccgcgtcgaccctc 17

RESULT 10

ID AAH48722 standard: DNA; 20 BP.

XX AAH48722;

DT 19-OCT-2001 (first entry)

DE Proto-oncogene bcl-2 associated primer SEQ ID 3.

XX KW Primer; phosphorothioate; somatostatin; cytostatic; virucide; asthma;
XX antiinflammatory; antisthmatic; cardiant; antineoplastic therapy;
XX cancer; viral disease; inflammatory process; somatostatin receptor;
XX central nervous system disease; cardiovascular disease; SSTR;
XX proto-oncogene; bcl-2; ss.

OS Unidentified.

XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= "OTHER"
FT /note= "phosphorothioate"

XX DE1006572-A1.

XX 23-AUG-2001.

XX 14-FEB-2000; 2000DE-1006572.

XX 14-FEB-2000; 2000DE-1006572.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Eisenhut M, Mier W, Ertia R, Haberhorn U;

XX WPI: 2001-530596/59.

XX New conjugates of oligonucleotides with somatostatin analogs, useful in
XX antisense therapy, e.g. of viral, inflammatory or asthmatic disease or
XX especially tumors overexpressing the somatostatin receptor -

XX Example 3; Page 9; 16pp; German.

XX This invention describes a novel oligonucleotide conjugate (I) comprising
XX (a) an oligonucleotide, at least part of the sequence of which is
XX complementary to part of an intracellular nucleic acid sequence; and (b)
XX a somatostatin analog. The products of the invention have cytostatic,
XX virucide, antiinflammatory, antisthmatic and cardiant activity. The use
XX of (I) is claimed in antisense therapy, especially of cancer, viral
XX disease, inflammatory processes or asthmatic, central nervous system or
XX cardiovascular disease. (I) are especially used for therapy of tumors
XX overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung
XX tumors, breast tumors, brain tumors or other endocrine tumors), but are
XX also useful for treating viral diseases (e.g. herpes simplex-1
XX infection), inflammatory disease (typical target RNA the NF-kappa-B),
XX asthmatic disease (typical target RNA the adenosine A1 receptor), central
XX nervous system disease (typical target RNA the dopamine receptor) or
XX cardiovascular disease (typical target RNA c-myc). (I) are efficiently
XX taken up by cells and incorporated in target cells (via the SSTR) and are
XX highly selective for cells overexpressing SSTRs. This sequence
XX represents a primer used to illustrate the method of the invention.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

XX Query Match 90.6%; Score 15.4; DB 22; Length 20;

XX Best Local Similarity 94.1%; Pred. No. 52;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 taccgcgtcgaccctc 17
DB 1 taccgcgtcgaccctc 17

RESULT 11

ID AA086552 standard: DNA; 17 BP.

XX AA086552;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

XX KW Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX lymphoma; programmed cell death; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc-feature 1..17
FT /*tag= a
FT /note= "3'-5' (antisense) sequence"

XX W09508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94MO-US10725.

XX 20-SEP-1993; 93US-0124256.

XX (REED/) REED J C.

XX Reed JC;

XX WPI: 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX of human solid tumors, esp. breast cancer

XX Example 12; Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce
XX programmed cell death (DNA fragmentation) in the human lymphoma cell
XX line RS11846. The oligonucleotides are phosphodiester targeted
XX against the translation initiation site (AA086550-55) or the 5'-cap
XX region (AA086556-58) of human bcl-2 pre-mRNAs. The AA086552
XX oligonucleotide provided pronounced DNA fragmentation.

XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

XX Query Match 82.4%; Score 14; DB 16; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtcgacc 14
DB 4 taccgcgtcgacc 17

XX 1 taccgcgtcgacc 14

RESULT 12

ID AA086550 standard: DNA; 17 BP.

XX AA086550;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX Lymphoma; programmed cell death; ss.
XX Synthetic.
XX OS
XX FH Key Location/Qualifiers
FT 1..17
FT misc-feature /*tag= a
FT /note= "3'-5' (antisense) sequence"
XX
XX PN W09508350-A.
XX
XX PD 30-MAR-1995.
XX
XX PF 20-SEP-1994; 94WO-US10725.
XX
XX PR 20-SEP-1993; 93US-0124256.
XX
XX PA (REED/) REED J C.
XX
XX PI Reed JC;
XX
XX DR WPI: 1995-139394/18.
XX
XX PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX PS Example 12; Page 33; 108pp; English.
XX
XX CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86650-55) of human bcl-2 pre-mRNAs.
XX
XX SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
Db 1 cgcgtgcgaccctc 14

RESULT 13
AAV28172
ID AAV28172 standard; DNA; 17 BP.
XX
XX AC AAV28172;
XX
XX DT 08-OCT-1998 (first entry)
XX
XX DE Antisense oligonucleotide to bcl-2 mRNA.
XX
XX KW Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
XX OS Synthetic.
XX
XX PN W09827425-A1.
XX
XX PD 25-JUN-1998.
XX
XX PF 18-DEC-1997; 97WO-US23284.
XX
XX PR 19-DEC-1996; 96US-0769951.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Chen D, Cole DL, Srivatsa GS;
PI

XX
XX DR WPI: 1998-362922/31.
XX
XX PT Matrix for selective separation of oligonucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
XX PS Disclosure; Page 79; 183pp; English.
XX
XX CC AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridising portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, for treating a non-pathogen,
XX non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX
XX SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
Db 1 cgcgtgcgaccctc 14

RESULT 14
AAV28173
ID AAV28173 standard; DNA; 17 BP.
XX
XX AC AAV28173;
XX
XX DT 08-OCT-1998 (first entry)
XX
XX DE Antisense oligonucleotide to bcl-2 mRNA.
XX
XX KW Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
XX OS Synthetic.
XX
XX PN W09827425-A1.
XX
XX PD 25-JUN-1998.
XX
XX PF 18-DEC-1997; 97WO-US23284.
XX
XX PR 19-DEC-1996; 96US-0769951.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Chen D, Cole DL, Srivatsa GS;
XX
XX DR WPI: 1998-362922/31.
XX
XX PT Matrix for selective separation of oligonucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
XX PS Disclosure; Page 79; 183pp; English.
XX
XX CC AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridising portion of the

CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 taccgcgtgcgacc 17

RESULT 15

AAV28174
ID AAV28174 standard; DNA; 17 BP.

AC AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97MO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 80; 183pp; English.

XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 taccgcgtgcgacc 17

Search completed: June 28, 2002, 22:40:13
Job time: 8089 sec

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rng

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.sz1m75.rn1

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:46 ; Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-9

Perfect score: 17

Sequence: 1 tacccgctgcagaccctc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	2	US-08-465-485A-9
2	17	100.0	17	3	US-09-080-285-9
3	17	100.0	18	4	US-09-030-701-28
4	17	100.0	18	4	US-09-286-098-60
5	17	100.0	18	4	US-08-960-774-60
6	17	82.4	17	2	US-08-465-485A-8
7	17	82.4	17	2	US-08-465-485A-10
8	14	82.4	17	3	US-09-080-285-8
9	14	82.4	17	3	US-09-080-285-10
10	14	69.4	18	3	US-08-953-664-1
11	11.8	69.4	18	3	US-08-953-664-2
12	11.8	69.4	18	4	US-09-487-874-1
13	11.8	69.4	18	4	US-09-487-874-2
14	11.4	67.1	31	1	US-08-095-726-25
15	11.4	67.1	31	1	US-08-095-726-27
16	11.4	67.1	31	1	US-08-096-043-22
17	11.4	67.1	31	1	US-08-096-043-24
18	11.4	67.1	31	1	US-08-093-577-18
19	11.4	67.1	31	1	US-08-093-577-20
20	11.4	67.1	31	1	US-08-096-623A-30
21	11.4	67.1	31	1	US-08-096-623A-32
22	11.2	65.9	19	4	US-09-038-637-97
23	11.2	65.9	28	1	US-08-049-264C-11
24	11.2	65.9	28	1	US-08-476-562-11
25	11.2	65.9	28	1	US-08-479-723A-11
26	11.2	65.9	28	5	PCR-US84-04310-11
27	11.2	65.9	32	4	US-08-913-014A-21

28	11.2	65.9	44	1	US-08-282-030-12	Sequence 12, Appl
29	11.2	65.9	44	5	PCR-US95-10219-12	Sequence 12, Appl
30	11.2	65.9	54	4	US-09-082-649B-14	Sequence 14, Appl
31	11.2	65.9	55	3	US-08-928-881-17	Sequence 17, Appl
32	11.2	65.9	59	1	US-08-282-030-14	Sequence 14, Appl
33	11.2	65.9	59	5	PCR-US95-10219-14	Sequence 14, Appl
34	11.2	65.9	69	3	US-08-928-881-15	Sequence 15, Appl
35	11.2	65.9	70	4	US-09-037-990B-53	Sequence 53, Appl
36	11	64.7	17	2	US-08-465-485A-11	Sequence 11, Appl
37	11	64.7	17	3	US-09-080-285-11	Sequence 11, Appl
38	11	64.7	17	4	US-09-025-763B-83	Sequence 83, Appl
39	10.8	63.5	22	4	US-09-311-260-60	Sequence 60, Appl
40	10.8	63.5	26	1	US-08-049-264C-56	Sequence 56, Appl
41	10.8	63.5	26	1	US-08-476-562-56	Sequence 56, Appl
42	10.8	63.5	26	1	US-08-479-723A-56	Sequence 56, Appl
43	10.8	63.5	26	5	PCR-US94-04310-56	Sequence 56, Appl
44	10.8	63.5	30	1	US-08-106-761-5	Sequence 5, Appl
45	10.8	63.5	30	4	US-08-918-148-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-9
Sequence 9, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-9

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 2

US-09-080-285-9
Sequence 9, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080.285
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 3
US-09-030-701-28
Sequence 28, Application US/09030701B
Patent No. 6214806
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
FILE REFERENCE: C1039/7011
CURRENT APPLICATION NUMBER: US/09/030.701B
PRIORITY FILING DATE: 1998-02-25
PRIORITY FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 4
US-09-286-098-60
Sequence 60, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286.098
PRIORITY FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-60

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 5

US-08-960-774-60
; Sequence 60, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieger et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-960-774-60

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgacccctc 17
|||
Db 1 TACCGCTGCACCCCTC 17

RESULT 6
US-08-465-485A-8
; Sequence 8, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-8

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgacccctc 17
|||
Db 1 CCGCTGCACCCCTC 14

RESULT 7
US-08-465-485A-10
; Sequence 10, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-10

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 TACCGCGTGCAC 17

RESULT 8
US-09-080-285-8
Sequence 8, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-8

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
DB 1 CGCGTGCACCTC 14

RESULT 9
US-09-080-285-10
Sequence 10, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-10

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtgcacc 14
|||||
DB 4 TACCGCGTCGAC 17

RESULT 10
US-08-952-664-1
Sequence 1, Application US/08952664
Patent No. 6034235

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, Haruo

APPLICANT: YAMAGAMI, Tamotsu

TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS

TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS

TITLE OF INVENTION: TUMOR GENE (WT1)

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,664

FILING DATE: 01-DEC-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/01394

FILING DATE: 24-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-156672

FILING DATE: 01-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wegner, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 053466/0223

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Synthetic DNA"

US-08-952-664-1

Query Match 69.4%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcaccct 16
|||||
DB 4 ACCGCATTCGACCT 18

RESULT 11

US-08-952-664-2/c
Sequence 2, Application US/08952664
Patent No. 6034235

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, Haruo

APPLICANT: YAMAGAMI, Tamotsu

APPLICANT: INOUE, Kazushi

TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS

TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS

TITLE OF INVENTION: TUMOR GENE (WT1)

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,664

FILING DATE: 01-DEC-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/01394

FILING DATE: 24-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-156672

FILING DATE: 01-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wegner, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 053466/0223

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Synthetic DNA"

US-08-952-664-2

Query Match 69.4%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcaccct 16
|||||
DB 15 ACCGCATTCGACCT 1

RESULT 12
US-09-487-874-1
Sequence 1, Application US/09487874
Patent No. 6277832

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, Haruo

APPLICANT: YAMAGAMI, Tamotsu

APPLICANT: INOUE, Kazushi

TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS

TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS

TITLE OF INVENTION: TUMOR GENE (WT1)

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/487,874
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,664
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-09-487-874-1

Query Match 69.4%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 accgcgtgcacct 16
||||| |||||
Db 4 ACCGCATTCGACCT 18

RESULT 13
US-09-487-874-2/c
Sequence 2, Application US/09487874
Patent No. 6277832
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Haruo
APPLICANT: YAMAGAMI, Tamotsu
APPLICANT: INOUE, Kazushi
TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS
TITLE OF INVENTION: COMPOSING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
TITLE OF INVENTION: TUMOR GENE (WT1)
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/487,874
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,664
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-09-487-874-2

Query Match 69.4%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 accgcgtgcacct 16
||||| |||||
Db 15 ACCGCATTCGACCT 1

RESULT 14
US-08-095-726-25
Sequence 25, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Hwei-Che B.
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, NO. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180

TELEFAX: 3128564972
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-095-726-25

Db 28
 CGCATGCCGACCT 16

Search completed: June 28, 2002, 22:16:47
 Job time: 8273 sec

Query Match 67.1%; Score 11.4; DB 1; Length 31;
 Best Local Similarity 92.3%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 cgcgtagcaccct 16
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 Db 4 CGCATGCCGACCT 16

RESULT 15
 US-08-095-726-27/c
 ; Sequence 27, Application US/08095726
 ; Patent No. 5530188
 ; GENERAL INFORMATION:
 ; APPLICANT: Ausich, Rodney L
 ; APPLICANT: Brinkhaus, Friedhelm L
 ; APPLICANT: Mukharji, Indrani
 ; APPLICANT: Proffitt, John H
 ; APPLICANT: Yarger, James G
 ; APPLICANT: Yen, Hui-Che B
 ; TITLE OF INVENTION: Beta-Carotene Biosynthesis in
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
 ; STREET: 200 E Randolph St
 ; CITY: Chicago
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60680-0703
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/095,726
 ; FILING DATE: 21-JUL-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/785,566
 ; FILING DATE: 30-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Galloway, No. 5530188val B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 3128567180
 ; TELEFAX: 3128564972
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-095-726-27

Query Match 67.1%; Score 11.4; DB 1; Length 31;
 Best Local Similarity 92.3%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 cgcgtagcaccct 16

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:06 ; Search time 3762.88 seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-10

Perfect score: 17

Sequence: 1 tctacgcgctgcgacc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 794432

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
1: gb_ba:
2: gb_htg:
3: gb_in:
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5: gb_ov:
6: gb_pat:
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8: gb_pl:
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11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
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22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htgo_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Match Length	ID	Description

1	17	100.0	17	6	AR052612	AR052612 Sequence
2	14	82.4	17	6	AR052611	AR052611 Sequence
3	14	82.4	17	6	AR052613	AR052613 Sequence
4	14	82.4	18	6	ARI46348	ARI46348 Sequence
5	14	82.4	18	6	ARI54731	ARI54731 Sequence
6	14	82.4	18	6	AXI03812	AXI03812 Sequence
7	14	82.4	18	6	AXI03864	AXI03864 Sequence
8	14	82.4	18	6	AX355457	AX355457 Sequence
9	14	82.4	18	6	BD009122	BD009122 Sequence
10	13.4	78.8	24	6	BD010808	BD010808 Sequence
11	12.2	71.8	27	6	AX049228	AX049228 Sequence
12	12.2	71.8	27	6	AX049833	AX049833 Sequence
13	12.2	71.8	27	6	AX050831	AX050831 Sequence
14	12.2	71.8	30	6	A12656	A12656 Sequence
15	12.2	71.8	30	6	ARI05729	ARI05729 Sequence
16	12.2	71.8	30	6	AX164810	AX164810 Sequence
17	11.8	69.4	26	6	AR003421	AR003421 Sequence
18	11.8	69.4	26	6	I21210	I21210 Sequence
19	11.8	69.4	26	6	I74477	I74477 Sequence
20	11.8	69.4	28	6	AR003376	AR003376 Sequence
21	11.8	69.4	28	6	I21165	I21165 Sequence
22	11.8	69.4	28	6	I74432	I74432 Sequence
23	11.8	69.4	35	6	AR003405	AR003405 Sequence
24	11.8	69.4	35	6	AR003406	AR003406 Sequence
25	11.8	69.4	35	6	I21194	I21194 Sequence
26	11.8	69.4	35	6	I21195	I21195 Sequence
27	11.8	69.4	35	6	I74461	I74461 Sequence
28	11.8	69.4	35	6	I74462	I74462 Sequence
29	11.8	69.4	36	6	AR003407	AR003407 Sequence
30	11.8	69.4	36	6	AR003408	AR003408 Sequence
31	11.8	69.4	36	6	I21196	I21196 Sequence
32	11.8	69.4	36	6	I21197	I21197 Sequence
33	11.8	69.4	36	6	I74463	I74463 Sequence
34	11.8	69.4	36	6	I74464	I74464 Sequence
35	11.8	69.4	45	6	AR003374	AR003374 Sequence
36	11.8	69.4	45	6	I21163	I21163 Sequence
37	11.8	69.4	45	6	I74430	I74430 Sequence
38	11.8	69.4	51	6	AR003378	AR003378 Sequence
39	11.8	69.4	51	6	I21167	I21167 Sequence
40	11.8	69.4	51	6	I74434	I74434 Sequence
41	11.8	69.4	56	6	AR003380	AR003380 Sequence
42	11.8	69.4	56	6	I21169	I21169 Sequence
43	11.8	69.4	56	6	I74436	I74436 Sequence
44	11.8	69.4	62	9	AB010683	AB010683 Homo sapi
45	11.8	69.4	71	9	HUMRPP70	D28411 Human mRNA

ALIGNMENTS

RESULT 1	AR052612	17 bp	DNA	Linear	PAT 29-SEP-1999
LOCUS	AR052612	Sequence	10 from patent US 5831066.		
DEFINITION	AR052612				
ACCESSION	AR052612				
VERSION	AR052612.1	GI:5975976			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Reed,J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A	10-03-NOV-1998;			
FEATURES	Location/Qualifiers				
source	1..17	/organism="unknown"			
BASE COUNT	2 a	8 c	4 g	3 t	
ORIGIN					

Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccctaccggtgcgacc 17
|||||
Db 1 TCCTACCGGTGCGACC 17

RESULT 2
AR052611
LOCUS AR052611 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccggtgcgacc 17
|||||
Db 1 TACCGGTGCGACC 14

RESULT 3
AR052613
LOCUS AR052613 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5831066.
ACCESSION AR052613
VERSION AR052613.1 GI:5975977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 11 03-NOV-1998;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"

BASE COUNT 1 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccctaccggtgcg 14
|||||
Db 4 TCCTACCGGTGCG 17

RESULT 4
AR146348
LOCUS AR146348 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION AR146348
VERSION AR146348.1 GI:15109537

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL Immunotherapeutic oligonucleotides and cytokines
FEATURES
source Patent: US 6218371-A 60 17-APR-2001;
1..18
Location/Qualifiers
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

QY 4 taccggtgcgacc 17
|||||
Db 1 TACCGGTGCGACC 14

RESULT 5
AR154731
LOCUS AR154731 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION AR154731
VERSION AR154731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccggtgcgacc 17
|||||
Db 1 TACCGGTGCGACC 14

RESULT 6
AX103812
LOCUS AX103812 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812
VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GMDH (DE)

FEATURES
source Location/Qualifiers
1..18

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
DB 1 TACCGCGTGCAC 14

RESULT 7
AX103864 18 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)

FEATURES
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
DB 1 TACCGCGTGCAC 14

RESULT 8
AX355457 18 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
DB 1 TACCGCGTGCAC 14

RESULT 9
BD009122 18 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Immunostimulatory nucleic acid molecules.
ACCESSION BD009122
VERSION BD009122.1 GI:18637495
KEYWORDS JP 2001503267-A/74.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PF 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEG,JOEL N KLINE
PC C07H21/00,C07H21/02,C07H21/04,A61K31/175,A61K31/335,A61K31/47,
A61K31/70

FEATURES
source 1..18
Location/Qualifiers
/organism="Artificial Sequence".
FT source 1..18

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
DB 1 TACCGCGTGCAC 14

RESULT 10
BD010808 24 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010808
VERSION BD010808.1 GI:18639181
KEYWORDS JP 2001069994-A/9.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito,T., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YURO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N3/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..24
Location/Qualifiers
1..24
/organism="Artificial Sequence"
/db_xref="taxon:32630"
BASE COUNT 5 a 10 c 5 g 4 t
ORIGIN

Query Match 78.8%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ctaccgcgtgcgacc 17
|||||
Db 1 CTACCGCGTGCGCC 15

RESULT 11
AX049228 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069896.
ACCESSION AX049228
VERSION AX049228.1 GI:12226046
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in hematopoietic cells
JOURNAL Patent: WO 0069896-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1..27
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 12
AX049833 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069898.
ACCESSION AX049833
VERSION AX049833.1 GI:12226261
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in allergy cells
JOURNAL Patent: WO 0069898-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1..27
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 13
AX050831 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069897.
ACCESSION AX050831
VERSION AX050831.1 GI:12226744
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in t cells
JOURNAL Patent: WO 0069897-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1..27
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 14
A12656 30 bp DNA linear PAT 10-DEC-1993
LOCUS
DEFINITION Oligonucleotide from patent w0606635.
ACCESSION A12656
VERSION A12656.1 GI:491432
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 30)
AUTHORS
TITLE ORAL VACCINES
JOURNAL Patent: WO 8606635-A 1 20-NOV-1986;
FEATURES
source 1..30
Location/Qualifiers

BASE COUNT 4 a 11 c 10 g 5 t
 ORIGIN /organism="synthetic construct"
 /db_xref="taxon:32630"

Query Match 71.8%; Score 12.2; DB 6; Length 30;
 Best Local Similarity 82.4%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 tctaccgcgtgagacc 17
 ||||| || |||||
 Db 10 TCCTACGCGCCTTCGACC 26

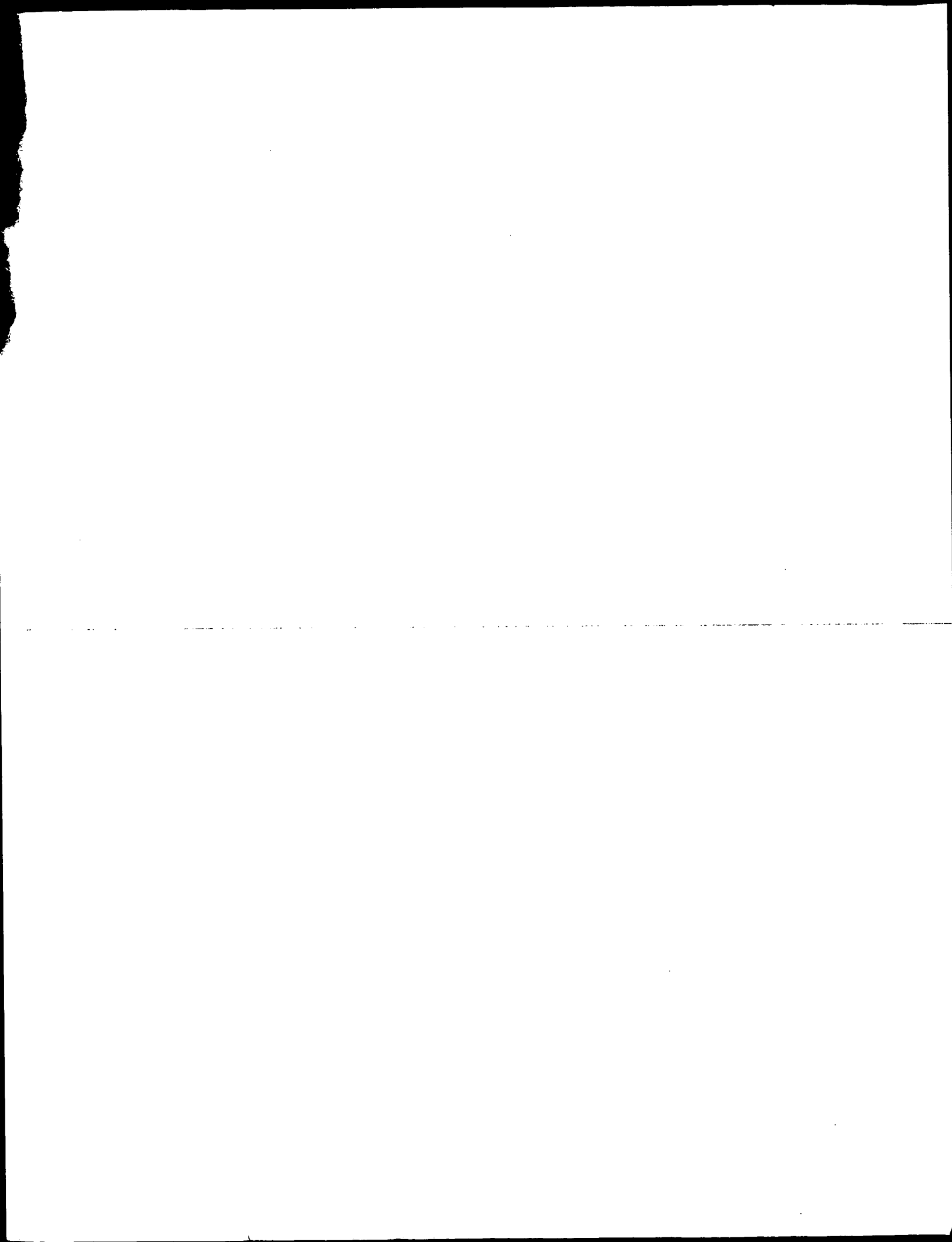
RESULT 15
 ARI05729
 LOCUS ARI05729 30 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 3 from patent US 6103243.
 ACCESSION ARI05729
 VERSION ARI05729.1 GI:12819794
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Russell-Jones, G. John, Howe, P., de Alzpurua, H. James and
 Rand, K. Norman.
 TITLE Oral vaccines
 JOURNAL Patent: US 6103243-A 3 15-AUG-2000;
 FEATURES Location/Qualifiers
 source 1..30
 /organism="unknown"

BASE COUNT 4 a 11 c 10 g 5 t
 ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 30;
 Best Local Similarity 82.4%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 tctaccgcgtgagacc 17
 ||||| || |||||
 Db 10 TCCTACGCGCCTTCGACC 26

Search completed: June 28, 2002, 22:11:07
 Job time: 8358 sec



DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086550-55) or the 5'-cap
CC region (AA086556-58) of human bcl-2 pre-mRNAs. The AA086552
CC oligonucleotide provided pronounced DNA fragmentation.

XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 17; DB 16; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
Db 1 tctaccgcgtgcgacc 17
|||||

RESULT 2

ID AAV28173 standard; DNA; 17 BP.

AC AAV28173;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

PI WPI; 1998-362922/31.

PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 79; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.

SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 17; DB 19; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
Db 1 tctaccgcgtgcgacc 17
|||||

RESULT 3

ID AAV28174 standard; DNA; 17 BP.

AC AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

PI WPI; 1998-362922/31.

PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 80; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.

SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 17; DB 19; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
Db 1 tctaccgcgtgcgacc 17
|||||

RESULT 4

AAV23685

ID AAX23685 standard; DNA: 17 BP.
XX
AC AAX23685;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 138.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI: 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 149; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 tctaccgctgcgacc 17
DB 1 tctaccgctgcgacc 17
XX
RESULT 5
AAX23686
ID AAX23686 standard; DNA: 17 BP.
XX
AC AAX23686;
XX

XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 139.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI: 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 149; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 tctaccgctgcgacc 17
DB 1 tctaccgctgcgacc 17
XX
RESULT 6
AAX18694
ID AAX18694 standard; DNA: 17 BP.
XX
AC AAX18694;
XX
DT 10-MAY-1999 (first entry)
XX

DE Target bcl-2 antisense oligonucleotide #26.
 XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
 KM alimentary canal; transport; gastrointestinal mucosa; cancer;
 KM Alzheimer's disease; beta-thalassemia; malaria; viral infection;
 KM HIV; inflammation; ss.
 XX Synthetic.
 OS
 PN WO9901579-A1.
 XX
 XX 14-JAN-1999.
 XX
 XX 01-JUL-1998; 98WO-US13574.
 XX
 XX 01-JUL-1997; 97US-0886829.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX Hardee G, Teng C;
 PI
 DR WPI; 1999-106077/09.
 XX
 XX Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability
 XX
 XX Example 2; Page 84; 115pp; English.
 PS
 XX A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.
 CC
 XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;
 SQ

Query Match 100.0%; Score 17; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
 |||||
 DB 1 tctaccgcgtgcgacc 17

RESULT 7
 AAX18695
 ID AAX18695 standard; DNA; 17 BP.
 XX
 XX AAX18695;
 AC
 XX 10-MAY-1999 (first entry)
 DE
 XX Target bcl-2 antisense oligonucleotide #27.
 DE
 XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
 KM alimentary canal; transport; gastrointestinal mucosa; cancer;
 KM Alzheimer's disease; beta-thalassemia; malaria; viral infection;
 KM HIV; inflammation; ss.
 XX

OS Synthetic.
 XX
 XX WO9901579-A1.
 PN
 XX 14-JAN-1999.
 PD
 XX
 XX 01-JUL-1998; 98WO-US13574.
 PF
 XX 01-JUL-1997; 97US-0886829.
 PR
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Hardee G, Teng C;
 PI
 DR WPI; 1999-106077/09.
 XX
 XX Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability
 XX
 XX Example 2; Page 85; 115pp; English.
 PS

A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.
 CC
 XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;
 SQ

Query Match 100.0%; Score 17; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
 |||||
 DB 1 tctaccgcgtgcgacc 17

RESULT 8
 AAQ86643
 ID AAQ86643 standard; DNA; 20 BP.
 XX
 XX AAQ86643;
 AC
 XX 27-SEP-1995 (first entry)
 DE
 XX Antisense oligomer TR-AS.
 DE
 XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KM leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
 KM ss.
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..20
 FT misc_feature
 FT /*tag= a
 FT /note= "3'-5' (antisense) sequence"
 XX
 XX WO9508350-A.
 PN

XX 30-MAR-1995.
PD 20-SEP-1994; 94WO-US10725.
XX 20-SEP-1993; 93US-0124256.
XX (REED/) REED J C.
XX Reed JC;
XX WPI; 1995-139394/18.
DR Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX Disclosure: Page 13; 108pp; English.
XX The antisense oligonucleotide T1-AS straddles the translation-
CC initiation site in the mRNA coding strand of the human bcl-2
CC gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
SQ
Query Match 94.1%; Score 16; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctaccgcgtgcgac 16
| | | | | | | | | | | | | | | | | | | | | |
Db 5 tctaccgcgtgcgac 20
RESULT 9
AAV28169
ID AAV28169 standard; DNA; 20 BP.
XX
XX AAV28169;
XX
XX 08-OCT-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
XX
XX Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
XX Synthetic.
XX
XX WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI; 1998-362922/31.
XX
XX Matrix for selective separation of oligo:nucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
XX Disclosure; Page 76; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that

CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
SQ
Query Match 94.1%; Score 16; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctaccgcgtgcgac 16
| | | | | | | | | | | | | | | | | | | | | |
Db 5 tctaccgcgtgcgac 20
RESULT 10
AAV23681
ID AAV23681 standard; DNA; 20 BP.
XX
XX AAV23681;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 134.
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.
XX
XX Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX
XX WPI; 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX
XX Example 9; Page 147; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
XX sensor arrays, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion sequence
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labeled and
XX hybridize with the probe oligonucleotides of the sensor arrays. Such
XX oligonucleotides and their targets are represented in AAV23548-X23709.
XX Oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion or
XX proliferation, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
XX Syncytial Virus or cytomegalovirus (CMV). The compositions enable

CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.

XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

SO Query Match

Best Local Similarity 94.1%; Score 16; DB 20; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16
|||||
Db 5 tctaccgcgtgcgac 20

RESULT 11

AA18690
ID AA18690 standard; DNA; 20 BP.

XX AAX18690;

XX 10-MAY-1999 (first entry)

XX Target bcl-2 antisense oligonucleotide #22.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
XX alimentary canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection;
XX HIV; inflammation; ss.

XX Synthetic.

XX MO9901579-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98MO-US13574.

XX 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

XX Hardee G, Teng C;

XX WPI; 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used
XX particularly for delivering therapeutic antisense oligonucleotides
XX across the gastrointestinal mucosa, provides high bioavailability
XX Example 2; Page 83; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a
XX nucleic acid and at least one penetration enhancer. The compositions are
XX used: (i) to treat or prevent any disease or disorder that can be
XX treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
XX beta-thalassemia, malaria, viral infections (including human immune
XX deficiency virus (HIV)), inflammation, in human or animal medicine;
XX (ii) to investigate the role of a gene or gene product in non-human
XX animals; and (iii) to modulate gene expression in cells, tissues or
XX organs. The compositions provide bioavailability of at least 15,
XX preferably 17-35%. The penetration enhancer improves: (i) transport of
XX the nucleic acid across the mucosa of the alimentary canal and into
XX cells; and (ii) increases stability of the nucleic acid. Oral
XX administration avoids the complications and expense of intravenous or
XX other methods of administration. AAX18690 to AAX18799 and AAX18801
XX represent antisense oligonucleotides which can be used as the nucleic
XX acid in the method of the invention.

SO Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

XX Query Match

Best Local Similarity 94.1%; Score 16; DB 20; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16
|||||
Db 5 tctaccgcgtgcgac 20

RESULT 12

AA249348
ID AA249348 standard; DNA; 20 BP.

XX AA249348;

XX 14-MAR-2000 (first entry)

XX bcl-2 targeted antisense oligonucleotide SEQ ID 13.

XX Cellular proliferation; expression; modulation; antisense;
XX non-parenteral; delivery; uptake; administration; emulsion;
XX ulcerative colitis; Crohn's disease; inflammatory bowel disease;
XX ss.

XX Synthetic.

XX Homo sapiens.

XX MO9960012-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99MO-US11394.

XX 21-MAY-1998; 98US-0082624.

XX (ISIS-) ISIS PHARM INC.

XX Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

XX WPI; 2000-072428/06.

XX New oligonucleotide compositions used for the non-parenteral delivery
XX of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular
XX decoys, external guide sequences or aptamers -
XX Example 2; Page 122; 133pp; English.

XX Sequences AA249344-249354, AA249384-249385, AA249387-249388 and
XX AA249392-249393 represent antisense oligonucleotides designed
XX to modulate the rate of cellular proliferation. The invention relates to
XX new compositions for the non-parenteral delivery of oligonucleotides
XX comprising at least one oligonucleotide in an emulsion. Oligonucleotides
XX delivered via the compositions of the invention can be used to modulate
XX expression of a cellular adhesion protein, modulate a rate of cellular
XX proliferation, or have biological activity against eukaryotic pathogens
XX or retroviruses. They can be used for treating conditions including
XX e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease
XX or undue cellular proliferation. The compositions can enhance the local
XX and systemic uptake and delivery of nucleic acids via non-parenteral
XX routes of administration (e.g., via the alimentary canal, skin, eyes,
XX pulmonary tract, urethra or vagina).

SO Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

XX Query Match

Best Local Similarity 94.1%; Score 16; DB 21; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16

Db 5 tctaccgcgtgcgac 20

RESULT 13

AAQ86651
ID AAQ86651 standard; DNA; 17 BP.

AC AAQ86651;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

OS Synthetic.

FT key Location/Qualifiers
FT misc_feature 1..17
FT /tag= a
FT /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
programmed cell death (DNA fragmentation) in the human lymphoma cell
line RSI1846. The oligonucleotides are phosphodiester targeted
against the translation initiation site (AAQ86650-55) or the 5'-cap
region (AAQ86656-58) of human bcl-2 pre-mRNAs. The AAQ86651
oligonucleotide provided pronounced DNA fragmentation.

CC oligonucleotide provided pronounced DNA fragmentation.

Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgcgtgcgac 17
|||||
Db 1 taccgcgtgcgac 14

RESULT 14

AAQ86653
ID AAQ86653 standard; DNA; 17 BP.

AC AAQ86653;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.
OS Synthetic.

FT key Location/Qualifiers
FT misc_feature 1..17
FT /tag= a
FT /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
programmed cell death (DNA fragmentation) in the human lymphoma cell
line RSI1846. The oligonucleotides are phosphodiester targeted
against the translation initiation site (AAQ86650-55) or the 5'-cap
region (AAQ86656-58) of human bcl-2 pre-mRNAs.

CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.

Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcg 14
|||||
Db 4 tctaccgcgtgcg 17

RESULT 15

AAV28175
ID AAV28175 standard; DNA; 17 BP.

AC AAV28175;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI: 1998-362922/31.

XX Matrix for selective separation of oligo:nucleotide - useful for,
 PT e.g. large scale purification of anti-sense agents from their
 PT deletion derivatives formed during synthesis

XX PS Disclosure: Page 81, 183pp: English.

XX AAV28155-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridising portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.

XX SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcctaccgcgtgcg 14
 |||||
 DB 4 tcctaccgcgtgcg 17

Search completed: June 28, 2002, 22:40:13
 Job time: 8089 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:47 ; Search time 334.55 Seconds
(without alignments)
12,482 Million cell updates/sec

Title: US-09-709-170A-10

Perfect score: 17

Sequence: 1 tctaccgcgtgcgacc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	2	US-08-465-485A-10
2	17	100.0	17	3	US-09-080-285-10
3	17	100.0	17	2	US-08-465-485A-9
4	14	82.4	17	2	US-08-465-485A-11
5	14	82.4	17	3	US-09-080-285-9
6	14	82.4	17	3	US-09-080-285-11
7	14	82.4	18	4	US-09-030-701-28
8	14	82.4	18	4	US-09-286-098-60
9	14	82.4	18	4	US-08-960-774-60
10	12.2	71.8	30	3	US-08-458-814-3
11	12.2	71.8	60	3	US-08-897-527-3
12	12.2	71.8	60	3	US-08-897-527-4
13	12.2	71.8	60	3	US-09-072-508-3
14	12.2	71.8	60	3	US-09-072-508-4
15	12.2	71.8	66	2	US-08-185-949B-85
16	12.2	71.8	75	3	US-08-897-527-2
17	12.2	71.8	75	3	US-09-072-508-2
18	11.8	69.4	26	1	US-08-049-264C-56
19	11.8	69.4	26	1	US-08-476-562-56
20	11.8	69.4	26	1	US-08-479-723A-56
21	11.8	69.4	26	5	PCT-US94-04310-56
22	11.8	69.4	28	1	US-08-049-264C-11
23	11.8	69.4	28	1	US-08-476-562-11
24	11.8	69.4	28	1	US-08-479-723A-11
25	11.8	69.4	28	5	PCT-US94-04310-11
26	11.8	69.4	35	1	US-08-049-264C-40
27	11.8	69.4	35	1	US-08-049-264C-41

ALIGNMENTS

28	11.8	69.4	35	1	US-08-476-562-40	Sequence 40, Appl
29	11.8	69.4	35	1	US-08-476-562-41	Sequence 41, Appl
30	11.8	69.4	35	1	US-08-479-723A-40	Sequence 40, Appl
31	11.8	69.4	35	1	US-08-479-723A-41	Sequence 41, Appl
32	11.8	69.4	35	5	PCT-US94-04310-40	Sequence 40, Appl
33	11.8	69.4	35	5	PCT-US94-04310-41	Sequence 41, Appl
34	11.8	69.4	36	1	US-08-049-264C-42	Sequence 42, Appl
35	11.8	69.4	36	1	US-08-049-264C-43	Sequence 43, Appl
36	11.8	69.4	36	1	US-08-476-562-42	Sequence 42, Appl
37	11.8	69.4	36	1	US-08-476-562-43	Sequence 43, Appl
38	11.8	69.4	36	1	US-08-479-723A-42	Sequence 42, Appl
39	11.8	69.4	36	1	US-08-479-723A-43	Sequence 43, Appl
40	11.8	69.4	36	5	PCT-US94-04310-42	Sequence 42, Appl
41	11.8	69.4	36	5	PCT-US94-04310-43	Sequence 43, Appl
42	11.8	69.4	45	1	US-08-049-264C-9	Sequence 9, Appl
43	11.8	69.4	45	1	US-08-476-562-9	Sequence 9, Appl
44	11.8	69.4	45	1	US-08-479-723A-9	Sequence 9, Appl
45	11.8	69.4	45	5	PCT-US94-04310-9	Sequence 9, Appl

RESULT 1
US-08-465-485A-10
Sequence 10, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-10

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgctgagacc 17
|||||
Db 1 TCCTACCGCTGCGACC 17

RESULT 2

US-09-080-285-10
; Sequence 10, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-10

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgctgagacc 17
|||||
Db 1 TCCTACCGCTGCGACC 17

RESULT 3
US-08-465-485A-9
; Sequence 9, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgctgagacc 17
|||||
Db 1 TACCGGCTGCGACC 14

RESULT 4
US-08-465-485A-11
; Sequence 11, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

Query Match 100.0%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-11

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcttaccgctgacg 14
|||||
DB 4 tcttaccgctgacg 17

RESULT 5
US-09-080-285-9
Sequence 9, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgctgacgacc 17
|||||
DB 1 taccgctgacgacc 14

RESULT 6
US-09-080-285-11
Sequence 11, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-11

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtgcgac 14
|||||
DB 4 TCCTACCGCTGCG 17

RESULT 7
US-09-030-701-28
Sequence 28, Application US/09030701B
Patent No. 6214806
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
FILE REFERENCE: C1039/7011
CURRENT APPLICATION NUMBER: US/09/030,701B
CURRENT FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/039,405
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgac 17
|||||
DB 1 taccgcgtgcgac 14

RESULT 8
US-09-286-098-60
Sequence 60, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: CYTOKINES
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-60

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgac 17
|||||
DB 1 taccgcgtgcgac 14

RESULT 9
US-08-960-774-60
Sequence 60, Application US/08960774
Patent No. 6239116
GENERAL INFORMATION:
APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-960-774-60

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgcgtgcgacc 17
|||||
DB 1 TACCGCGTCGACC 14

RESULT 10

US-08-458-814-3
Sequence 3, Application US/08458814
Patent No. 6103243
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J
APPLICANT: DE AIZPURA, Henry J
APPLICANT: HOME, Peter
APPLICANT: RAND, Keith N
TITLE OF INVENTION: ORAL VACCINES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,814
FILING DATE: 02-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/327,822
FILING DATE: 18-OCT-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US086/00135
FILING DATE: 14-MAY-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH3104
FILING DATE: 25-OCT-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH0566
FILING DATE: 15-MAY-1985
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/155/BIAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-458-814-3

Query Match 71.8%; Score 12.2; DB 3; Length 30;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 tctaccgcgtgcgacc 17

|||||
DB 10 TCTACGCGCTTCGACC 26

RESULT 11

US-08-897-527-3/c
Sequence 3, Application US/08897527
Patent No. 6013770
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
APPLICANT: Zhang, Yuzhi
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,527
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-4"
US-08-897-527-3

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
|||||
DB 36 TCTACGCGCTTCGACC 20

RESULT 12

US-08-897-527-4/c
Sequence 4, Application US/08897527
Patent No. 6013770
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
APPLICANT: Zhang, Yuzhi
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,527
FILING DATE:
CLASSIFICATION: 51A
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-5"
US-08-897-527-4

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgctgcgacc 17
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DB 36 TCCTACGGCCTGCGGCC 20

RESULT 13
US-09-072-508-3/C
Sequence 3, Application US/09072508
Patent No. 6045799
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,508
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-4"
US-09-072-508-3

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgctgcgacc 17
||||| ||||| ||
DB 36 TCCTACGGCCTGCGGCC 20

RESULT 14
US-09-072-508-4/C
Sequence 4, Application US/09072508
Patent No. 6045799
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,508
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-5"

US-09-072-508-4

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgctgcgacc 17
||||| ||||| ||
DB 36 TCCTACGGCCTGCGGCC 20

RESULT 15
US-08-185-949B-85
Sequence 85, Application US/08185949B

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; Patent No. 5874279
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; APPLICANT: Richard D. Macdonald
; TITLE OF INVENTION: Recombinant Infectious Bovine
; TITLE OF INVENTION: Rhinotracheitis Virus
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,949B
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 278-0525
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-185-949B-85

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Query Match          71.8%; Score 12.2; DB 2; Length 66;
Best Local Similarity 82.4%; Pred. NO. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 tctaccgctgagacc 17
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Db 15 TCCTGCGCGCGCGGCC 31

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Search completed: June 28, 2002, 22:16:47
Job time: 8273 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:07 ; Search time 3762.88 Seconds
(without alignments)
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Title: US-09-709-170A-11

Perfect score: 17
Sequence: 1 cctctaccgcgctgcg 17

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb.ba:*
2: gb.htg:*
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12: gb.sy:*
13: gb.un:*
14: gb.vl:*
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29: em.vl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Query Length	DB ID	Description
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1	17	100.0	17	6	AR052613	AR052613 Sequence
2	14	82.4	17	6	AR052612	AR052612 Sequence
3	14	82.4	17	6	AR052614	AR052614 Sequence
4	12.8	75.3	52	9	S63038	S63038 T cell rece
5	12.8	75.3	68	6	AX195437	AX195437 Sequence
6	12.2	71.8	37	6	AR121243	AR121243 Sequence
7	12.2	71.8	50	6	AX159278	AX159278 Sequence
8	12.2	71.8	51	9	HS413212	AX132122 Homo sapi
9	12	70.6	24	6	BD010808	BD010808 Novel pol
10	11.8	69.4	18	12	AKM228027	AKJ229027 Artificial
11	11.8	69.4	24	6	AR097986	AK097986 Sequence
12	11.8	69.4	26	6	AR116948	AK116948 Sequence
13	11.8	69.4	26	6	AR148920	AR148920 Sequence
14	11.8	69.4	28	6	AR148922	AR148922 Sequence
15	11.8	69.4	28	6	AR148927	AR148927 Sequence
16	11.8	69.4	30	6	AX003496	AX003496 Sequence
17	11.8	69.4	48	6	AX274545	AX274545 Sequence
18	11.4	67.1	28	6	AR122834	AR122834 Sequence
19	11.4	67.1	28	6	AR122835	AR122835 Sequence
20	11.4	67.1	29	6	AR122852	AR122852 Sequence
21	11.4	67.1	29	6	AR122853	AR122853 Sequence
22	11.4	67.1	29	6	AR122855	AR122855 Sequence
23	11.4	67.1	29	6	AR122855	AR122855 Sequence
24	11.4	67.1	30	6	AR122833	AR122833 Sequence
25	11.4	67.1	31	6	AX158311	AX158311 Sequence
26	11.4	67.1	51	6	AX158312	AX158312 Sequence
27	11.4	67.1	51	6	AX158313	AX158313 Sequence
28	11.4	67.1	51	6	AX158314	AX158314 Sequence
29	11.4	67.1	61	6	AR122795	AR122795 Sequence
30	11.4	67.1	61	6	AR122800	AR122800 Sequence
31	11.4	67.1	74	9	S59798517	S59817 PKLR-L-type
32	11.2	65.9	20	6	AX191328	AX191328 Sequence
33	11.2	65.9	22	6	AR106739	AR106739 Sequence
34	11.2	65.9	24	6	AR149569	AR149569 Sequence
35	11.2	65.9	24	6	AX290693	AX290693 Sequence
36	11.2	65.9	28	6	A40136	A40136 Sequence 12
37	11.2	65.9	28	6	AR089991	AR089991 Sequence
38	11.2	65.9	34	6	A40128	A40128 Sequence 4
39	11.2	65.9	45	6	A17138	A17138 Oligonucleo
40	11.2	65.9	45	6	AR027521	AR027521 Sequence
41	11.2	65.9	60	6	AR009386	AR009386 Sequence
42	11.2	65.9	62	9	AB010683	AB010683 Homo sapi
43	11.2	65.9	74	9	D86110	D86110 Homo sapien
44	11	64.7	17	6	AR052611	AR052611 Sequence
45	11	64.7	17	6	AR052615	AR052615 Sequence

ALIGNMENTS

RESULT 1	AR052613	AR052613	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence	11 from patent US 5831066.				
DEFINITION	AR052613					
ACCESSION	AR052613.1	GI:5975977				
VERSION						
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 17)					
AUTHORS	Reed,J.C.					
TITLE	Regulation of bcl-2 gene expression					
JOURNAL	Patent: US 5831066-A 11 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1..17					
BASE COUNT	1 a 8 c 4 g 4 t					
ORIGIN	/organism="unknown"					

Query Match	100.0%;	Score 17;	DB 6;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 3e+02;		

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctg 17
Db 1 CCTTCTACCGCGTCCG 17

RESULT 2
LOCUS AR052612 17 bp DNA
DEFINITION Sequence 10 from patent US 5831066.
ACCESSION AR052612
VERSION AR052612.1 GI:5975976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of hcl-2 gene expression
JOURNAL Patent: US 5831066-A 10-03-NOV-1998;
FEATURES
source 1..17
/organism="unknown"

BASE COUNT 2 a 8 c 3 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctctaccgctg 17
Db 1 TCTTCTACCGCGTCCG 14

RESULT 3
LOCUS AR052614 17 bp DNA
DEFINITION Sequence 12 from patent US 5831066.
ACCESSION AR052614
VERSION AR052614.1 GI:5975978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of hcl-2 gene expression
JOURNAL Patent: US 5831066-A 12-03-NOV-1998;
FEATURES
source 1..17
/organism="unknown"

BASE COUNT 2 a 8 c 3 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctg 14
Db 4 CCTTCTACCGCGT 17

RESULT 4
LOCUS S63038 52 bp DNA
DEFINITION T cell receptor V delta 1-J delta 1 junction (sample 127) [human,
adult, genomic, 52 nt].
ACCESSION S63038

VERSION S63038.1 GI:386400
KEYWORDS human adult.
SOURCE Homo sapiens
ORGANISM
REFERENCE 1 (bases 1 to 52)
AUTHORS Beldford,K., Beldford,C., MacIntyre,E., Even,P. and Sigaux,F.
TITLE Peripheral selection of V delta 1+ cells with restricted T cell
receptor delta gene junctional repertoire in the peripheral blood
of healthy donors
JOURNAL J. Exp. Med. 178 (1), 121-127 (1993)
MEDLINE 93301588
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI g1bbsg 134205] from the original journal article.
This sequence comes from fig. 2.

FEATURES
source 1..52
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..52
/partial
/gene="T cell receptor V delta 1-J delta 1 junction"

BASE COUNT 10 a 17 c 11 g 14 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 9; Length 52;
Best Local Similarity 87.5%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctctaccgctg 16
Db 20 CCTTCTACCGCGTCC 35

RESULT 5
LOCUS AX195437 68 bp DNA
DEFINITION Sequence 36 from Patent WO0151646.
ACCESSION AX195437
VERSION AX195437.1 GI:15385983
KEYWORDS
SOURCE Aspergillus oryzae.
ORGANISM Aspergillus oryzae
REFERENCE 1 (bases 1 to 68)
AUTHORS Yaver,D.S. and Bellini,D.A.
TITLE Methods for producing a polypeptide using a crippled translational
initiator sequence
JOURNAL Patent: WO 0151646-A 36-19-JUL-2001;
FEATURES
source 1..68
Location/Qualifiers
/organism="Aspergillus oryzae"
/db_xref="taxon:5062"

BASE COUNT 16 a 13 c 24 g 15 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 9; Length 68;
Best Local Similarity 87.5%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cctctaccgctg 17
Db 3 CTTCCTACCGCGTCCG 18

RESULT 6
LOCUS ARI21243 37 bp DNA
DEFINITION T cell receptor V delta 1-J delta 1 junction (sample 127) [human,
adult, genomic, 52 nt].
ACCESSION ARI21243

DEFINITION Sequence 23 from patent US 6159710.
ACCESSION AR121243
VERSION AR121243.1 GI:14104819
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 37)
AUTHORS Fraser,N.W., Zabolotny,J.M. and Krummenacher,C.F.
TITLE Method and compositions for stabilizing unstable gene transcripts
JOURNAL Patent: US 6159710-A 23 12-DEC-2000;
FEATURES
source
BASE COUNT 5 a 18 c 10 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcctacgcgctgcg 17
||| ||| ||| ||| |||
Db 6 CCTCCTCCTCCGCGGCGC 22

RESULT 7
AX159278 AX159278 50 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 2606 from Patent WO0140521.
DEFINITION AX159278
ACCESSION AX159278
VERSION AX159278.1 GI:14540609
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2606 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number c94106315"
misc-feature
26
/note="2 of 2 allelic variants (2605 is other entry)"
BASE COUNT 6 a 21 c 12 g 11 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 50;
Best Local Similarity 82.4%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcctacgcgctgcg 17
||| ||| ||| ||| |||
Db 13 CCTTCTCTCTCGCTGCG 29

RESULT 8
HSA12122
LOCUS HSA12122 51 bp mRNA linear PRI 06-MAR-2000
DEFINITION Homo sapiens mRNA for T-cell receptor delta chain, CDR3 region
clone D28.
ACCESSION AJ132122
VERSION AJ132122.1 GI:4151017

KEYWORDS T-cell receptor delta; TCR delta chain.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Jouen-Beades,F., Halary,F., Drouot,L., Peyrat,M.A., Paris,E.,
Joly,P., Gilbert,D., Bonneville,M. and Tron,F.
TITLE Expansion of circulating V gamma 9/V delta 1 T cells in a patient
with a syndrome of recurrent fever: evidence for an unusual
antigen-driven process leading to selection of recurrent motifs
within TCR junctional loops of diverse lengths
JOURNAL Eur.J Immunol. 29 (10), 3338-3349 (1999)
MEDLINE 20010072
REFERENCE 2 (bases 1 to 51)
AUTHORS Jouen-Beades,F.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1999) Jouen-Beades F., Immunologie, INSERM U519,
Faculte de Medecine, 22 boulevard Gambetta, 76183 Rouen cedex,
FRANCE
FEATURES
source
Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="D28"
/rearranged
<1..>51
/codon_start=1
/product="T-cell receptor delta chain, CDR3 region"
/protein_id="CAI10585.1"
/db_xref="GI:4151018"
/translation="LGERRAFLRGCGIRADK"
BASE COUNT 11 a 10 c 21 g 9 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 9; Length 51;
Best Local Similarity 82.4%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcctacgcgctgcg 17
||| ||| ||| ||| |||
Db 17 CCTTCTCTCGGCTGCG 33

RESULT 9
BD010808
LOCUS BD010808 24 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010808
VERSION BD010808.1 GI:18639181
KEYWORDS JP 2001069994-A/9.
SOURCE Synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR

PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//

PC C12P21/08.C12N15/00.A61K37/02.C12N5/00
CC Key Location/Qualifiers
FH source 1..24
FT /organism='Artificial Sequence',
Location/Qualifiers
FEATURES
source 1..24
/organism='synthetic construct'
/db_xref='taxon:32630'
BASE COUNT 5 a 10 c 5 g 4 t
ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ctaccgcgtg 17
|||||
DB 1 CTACCGCGTGC 12

RESULT 10
AMM229027/c 18 bp DNA linear SYN 09-NOV-1998
LOCUS Artificial Apis mellifera mellifera microsatellite PCR primer
DEFINITION
AP19-2.
ACCESSION AJ229027
VERSION AJ229027.1 GI:3858924
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baudry,E., Solignac,M., Garnery,L., Gries,M., Cornuet,J.M. and Koeniger,N.
TITLE Relatedness among honey bees of a drone congregation and its sociobiological consequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 18)
AUTHORS Solignac,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1998) Solignac M., Laboratoire PGE, CNRS, Avenue de la Terrasse, 91198 Gif-sur-Yvette cedex, FRANCE
FEATURES
source 1..18
/organism='synthetic construct'
/db_xref='taxon:32630'
primer_bind 1..18
/note='PCR primer used to amplify Apis mellifera ssp. mellifera microsatellite locus Ap19'
/PCR_conditions='annealing temperature: 56 degC, MgCl2 concentration: 1.2 mM, length fragment 136 bp.'
BASE COUNT 6 a 3 c 7 g 2 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 12; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctcaccgctgc 16
|||||
DB 17 CTCTCACC GCGTAC 3

RESULT 11
AR097986 24 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 1 from patent US 6074823.
ACCESSION AR097986
VERSION AR097986.1 GI:12807243
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Koster,H.
TITLE DNA sequencing by mass spectrometry via exonuclease degradation
JOURNAL Patent: US 6074823-A 1 13-JUN-2000;
Location/Qualifiers
FEATURES
source 1..24
/organism='unknown'
BASE COUNT 6 a 9 c 4 g 5 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctctcaccgctg 15
|||||
DB 3 CATTCACCGCGTGC 17

RESULT 12
AR116948 24 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 1 from patent US 6140053.
ACCESSION AR116948
VERSION AR116948.1 GI:14097854
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Koster,H.
TITLE DNA sequencing by mass spectrometry via exonuclease degradation
JOURNAL Patent: US 6140053-A 1 31-OCT-2000;
Location/Qualifiers
FEATURES
source 1..24
/organism='unknown'
BASE COUNT 6 a 9 c 4 g 5 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctctcaccgctg 15
|||||
DB 3 CATTCACCGCGTGC 17

RESULT 13
AR148920 26 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 19 from patent US 6225531.
ACCESSION AR148920
VERSION AR148920.1 GI:15113010
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kakitani,M., Umemoto,N., Ishida,I., Iwamatsu,A., Yoshikawa,M. and Yamaoka,N.
TITLE Glucan elicitor receptor, DNA molecule coding therefor, and fungus-resistant plants transformed with the DNA molecule and method for creating the plants
JOURNAL Patent: US 6225531-A 19 01-MAY-2001;
Location/Qualifiers
FEATURES
source 1..26
/organism='unknown'

BASE COUNT 7 a 5 c 10 g 4 t
ORIGIN

Query Match

Best Local Similarity 69.4%; Score 11.8; DB 6; Length 26;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgctgc 16
|||||||
Db 26 CTCTCTACCCCATGC 12

QY 2 ctctctaccgctgc 16
|||||||
Db 11 CTCTCTACCCCATGC 25
Search completed: June 28, 2002, 22:11:09
Job time: 8360 sec

RESULT 14

ARI48922 ARI48922 28 bp DNA linear PAT 08-AUG-2001
LOCUS DEFINITION Sequence 21 from patent US 6225531.
ACCESSION ARI48922
VERSION ARI48922.1 GI:15113012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kakitani, M., Umemoto, N., Ishida, I., Iwamatsu, A., Yoshikawa, M. and Yamaoka, N.

TITLE

Glucan elicitor receptor, DNA molecule coding therefor,
fungus-resistant plants transformed with the DNA molecule and
method for creating the plants
Patent: US 6225531-A 21 01-MAY-2001;
Location/Qualifiers

JOURNAL
FEATURES
SOURCE 1..28
/organism="unknown"

BASE COUNT 5 a 10 c 5 g 8 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 28;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgctgc 16
|||||||
Db 11 CTCTCTACCCCATGC 25

RESULT 15

ARI48927 ARI48927 28 bp DNA linear PAT 08-AUG-2001
LOCUS DEFINITION Sequence 26 from patent US 6225531.
ACCESSION ARI48927
VERSION ARI48927.1 GI:15113017
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kakitani, M., Umemoto, N., Ishida, I., Iwamatsu, A., Yoshikawa, M. and Yamaoka, N.

TITLE

Glucan elicitor receptor, DNA molecule coding therefor,
fungus-resistant plants transformed with the DNA molecule and
method for creating the plants
Patent: US 6225531-A 26 01-MAY-2001;
Location/Qualifiers

JOURNAL
FEATURES
SOURCE 1..28
/organism="unknown"

BASE COUNT 5 a 10 c 5 g 8 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 28;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Mon Jul 1 08:40:45 2002

us-09-709-170a-11.szlm75.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:13 ; Search time 1381.16 Seconds
(without alignments)
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Title: US-09-709-170A-11

Perfect score: 17

Sequence: 1 cctcctaccgcgtgcg 17

Scoring table: IDENTITY NUC

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	AA086653	Bcl-2 antisense ol
2	17	100.0	17	AAV28175	Antisense oligonuc
3	17	100.0	17	AAV23687	Deletion sequence
4	17	100.0	17	AAV18696	Target bcl-2 antis
5	17	100.0	20	AAQ86643	Antisense oligomer
6	17	100.0	20	AAV28169	Antisense oligonuc
7	17	100.0	20	AAV23681	Deletion sequence
8	17	100.0	20	AAV18690	Target bcl-2 antis
9	17	100.0	20	AAZ49348	bcl-2 targeted an

10	14	82.4	17	16	AA086652	Bcl-2 antisense ol
11	14	82.4	17	16	AA086654	Bcl-2 antisense ol
12	14	82.4	17	19	AAV28173	Antisense oligonuc
13	14	82.4	17	19	AAV28174	Antisense oligonuc
14	14	82.4	17	19	AAV28176	Antisense oligonuc
15	14	82.4	17	20	AAV23688	Deletion sequence
16	14	82.4	17	20	AAV23686	Deletion sequence
17	14	82.4	17	20	AAV23685	Deletion sequence
18	14	82.4	17	20	AAV18694	Target bcl-2 antis
19	14	82.4	17	20	AAV18695	Target bcl-2 antis
20	14	82.4	17	20	AAV18697	Target bcl-2 antis
21	13	76.5	19	17	AAV27370	Anti-ras oncogene
22	12.8	75.3	68	22	AAV08593	Aspergillus niger
23	12.2	71.8	24	19	AAV62489	Op 1e2 gene pa sig
24	12.2	71.8	25	19	AAV62494	Op 1e2 gene pa sig
25	12.2	71.8	28	18	AAV06292	Type XIII collagen
26	12.2	71.8	37	19	AAV64925	HSV-1 primer PEPB8
27	12.2	71.8	45	15	AAV070687	Purine rich region
28	12.2	71.8	50	22	AAV75665	Human silent SNP c
29	12.2	71.8	54	19	AAV64900	HSV-1 latency asso
30	12	70.6	19	19	AAV70263	Human HMGI-C mRNA
31	12	70.6	24	22	AAV59071	MVP related PCR pr
32	12	70.6	33	12	AAQ10110	Probe 1479 to Chla
33	11.8	69.4	17	21	AAV06292	Hammerhead ribozym
34	11.8	69.4	20	20	AAV95174	PCR primer used to
35	11.8	69.4	21	19	AAZ25856	Human polymorphic
36	11.8	69.4	26	17	AAV09997	Primer for amplifi
37	11.8	69.4	26	18	AAV74651	PCR primer U37 SBQ
38	11.8	69.4	26	19	AAV29167	Nucleotide sequenc
39	11.8	69.4	28	17	AAV09999	Primer for amplifi
40	11.8	69.4	28	17	AAV10844	Primer for amplifi
41	11.8	69.4	28	18	AAV74653	PCR primer U37 SBQ
42	11.8	69.4	30	20	AAV1662	Probe used to isol
43	11.8	69.4	32	20	AAV90786	Primer Y152R. Sy
44	11.8	69.4	36	21	AAV5739	permutated linker e
45	11.8	69.4	50	22	AAV28176	Human SNP oligonuc

ALIGNMENTS

RESULT 1	
AA086653	AA086653 standard; DNA; 17 BP.
ID	
XX	AA086653;
AC	27-SEP-1995 (first entry)
XX	
DT	Bcl-2 antisense oligonucleotide.
XX	
DE	
XX	
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	
OS	Synthetic.
XX	
PH	Key
FT	misc-feature
FT	Location/Qualifiers
FT	1.17
FT	/*tag= a
FT	/note= "3'-5' (antisense) sequence"
XX	
XX	W09508350-A.
XX	
XX	30-MAR-1995.
XX	
XX	20-SEP-1994; 94WO-US10725.
XX	
XX	20-SEP-1993; 93US-0124256.
XX	
XX	(REED/) REED J C.
XX	
XX	Reed JC;
XX	

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086650-55) or the 5'-cap
CC region (AA086656-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgtgcg 17
1 ||||||||||||
Db 1 cctctaccgcgtgcg 17

RESULT 2
AAV28175
ID AAV28175 standard; DNA; 17 BP.
XX
AC AAV28175;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KW Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
PT WPI; 1998-362922/31.
XX
DR Matrix for selective separation of oligonucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
PS Disclosure; Page 81; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgtgcg 17
1 ||||||||||||
Db 1 cctctaccgcgtgcg 17

RESULT 3
AAV23687
ID AAV23687 standard; DNA; 17 BP.
XX
AC AAV23687;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 140.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
PT WPI; 1999-205198/17.
XX
DR New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX
PS Example 9; Page 150; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen or a
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including Influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

[illegible]

```
XX XX WPI; 1999-205198/17.
```

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DR
```

```
XX New compositions comprising sensor arrays made up of unique probe
```

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PT oligonucleotides - useful for characterizing a sample of target
```

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PT deletion oligonucleotides
```

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PS
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```
XX Example 9; Page 147; 163pp; English.
```

This invention describes a novel composition comprising a number of
sensor arrays, where each array comprises a unique probe or
CC oligonucleotide, which is the reverse complement of part of a unique
target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
sample of target deletion oligonucleotides which are labelled and
hybridize with the probe oligonucleotides of the sensor arrays. Such
oligonucleotides and their targets are represented in AAX23548-x23709.
Oligonucleotides characterized by the method form pharmaceutical
compositions that are useful for modulating cellular adhesion or
cell proliferation, and being active against a eukaryotic pathogen, a human
retrovirus, a human immunodeficiency virus (HIV), or a non-human
retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
Syncytial Virus or cytomegalovirus (CMV). The compositions enable
characterization of deletion sequence oligonucleotides having related,
but different nucleobase sequences, and quantification of different
species of deletion sequence ("target") oligonucleotides in a mixture.
Also, if the specificity of the oligonucleotide's nucleobase sequence
for its reverse complement is not modified, the method may be performed
using oligodeoxynucleotides.

```
SC Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;
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Query Match 100.0%; Score 17; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY     1 ccttccacgcgctcgcg 17  
        |||iiiiiiiii||  
Db     2 ccttcactcgctgcgcg 18
```

RESULT 8
AAXI8690
ID AAXI8690 standard; DNA; 20 BP.

AAXI8690;

```
XX  
XX  
DT     10-MAY-1999 (first entry)  
DE Target bcl-2 antisense oligonucleotide #22.
```

```
KW Cellular adhesion protein; proliferation; antisense oligonucleotide;  
alimentary canal; transport; gastrointestinal mucosa; cancer;  
Alzheimer's disease; beta-thalassemia; malaria; viral infection;  
HIV; inflammation; ss.
```

```
KW  
OS Synthetic.  
XX  
PN WO9901579-A1.  
PD 14-JAN-1999.  
PE 01-JUL-1998; 98WO-US13574.  
PR 01-JUL-1997; 97US-0886829.  
PA (ISIS-) ISIS PHARM INC.
```

```
PJ Hardee G, Teng C;  
XR WPI; 1999-106077/09.
```

PT Composition comprising nucleic acid and penetration enhancer - used
PT particularly for delivering therapeutic antisense oligonucleotides
PT across the gastrointestinal mucosa, provides high bioavailability
XX
PS Example 2; Page 83; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC treated: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAX18669 to AAX18799 and AAX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgctgcg 17
|||||
DB 2 cctctaccgcgctgcg 18

RESULT 9

AAZ49348
ID AAZ49348 standard; DNA; 20 BP.

XX
XX AAZ49348;

DT 14-MAR-2000 (first entry)

DE bcl-2 targeted antisense oligonucleotide SEQ ID 13.

XX Cellular proliferation; expression; modulation; antisense;

KW non-parenteral; delivery; uptake; administration; emulsion;

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;

SS.

XX
OS Synthetic.

OS Homo sapiens.

XX
PN WO960012-A1.

XX
PD 25-NOV-1999.

XX
PF 20-MAY-1999; 99WO-US11394.

XX
PR 21-MAY-1998; 98US-0082624.

XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

XX
DR WPI; 2000-072428/06.

XX
XX New oligonucleotide compositions used for the non-parenteral delivery
XX of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular
XX decoys, external guide sequences or aptamers -
XX
XX Example 2; Page 122; 133pp; English.

CC Sequences AAZ49344-249354, AAZ49384-249385, AAZ49387-249388 and
CC AAZ49392-249393 represent antisense oligonucleotides designed
CC to modulate the rate of cellular proliferation. The invention relates to
CC new compositions for the non-parenteral delivery of oligonucleotides
CC comprising at least one oligonucleotide in an emulsion. Oligonucleotides
CC delivered via the compositions of the invention can be used to modulate
CC expression of a cellular adhesion protein, modulate a rate of cellular
CC proliferation, or have biological activity against eukaryotic pathogens
CC or retroviruses. They can be used for treating conditions including
CC e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease
CC or undue cellular proliferation. The compositions can enhance the local
CC and systemic uptake and delivery of nucleic acids via non-parenteral
CC routes of administration (e.g., via the alimentary canal, skin, eyes,
CC pulmonary tract, urethra or vagina).

XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgctgcg 17
|||||
DB 2 cctctaccgcgctgcg 18

RESULT 10
AAQ86652
ID AAQ86652 standard; DNA; 17 BP.

XX
XX AAQ86652;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

XX Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT misc_feature 1..17

FT /tag= 2
/note= "3'-5' (antisense) sequence"

XX
PN WO9508350-A.

XX
PD 30-MAR-1995.

XX
PF 20-SEP-1994; 94WO-US10725.

XX
PR 20-SEP-1993; 93US-0124256.

XX
PA (REED/) REED J C.

XX
PI Reed JC;

XX
DR WPI; 1995-139394/18.

XX
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX of human solid tumours, esp. breast cancer

XX
PS Example 12; Page 33; 108pp; English.

XX
XX Antisense oligonucleotides were tested for their ability to induce
XX programmed cell death (DNA fragmentation) in the human lymphoma cell
XX line RS11846. The oligonucleotides are phosphodiester targeted
XX against the translation initiation site (AAQ86650-55) or the 5'-cap
XX region (AAQ86656-58) of human bcl-2 pre-mRNAs. The AAQ86652
XX oligonucleotide provided pronounced DNA fragmentation.

Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctaccgcgtgcg 17
|||||
Db 1 tctaccgcgtgcg 14

RESULT 11

AA086654
ID AA086654 standard; DNA; 17 BP.

AC AA086654;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss.

OS Synthetic.

FT Key location/Qualifiers

FT misc_feature 1..17
/tag= 2
/note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce

CC programmed cell death (DNA fragmentation) in the human lymphoma cell

CC line RS11846. The oligonucleotides are phosphodiester targeted

CC against the translation initiation site (AA086650-55) or the 5'-cap

CC region (AA086656-58) of human bcl-2 pre-mRNAs.

SO Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

QY 1 ccttcctaccgcgt 14
|||||

Db 4 ccttcctaccgcgt 17

RESULT 12

AAV28173
ID AAV28173 standard; DNA; 17 BP.

AC AAV28173;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PE 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligonucleotide - useful for,

PT e.g. large scale purification of anti-sense agents from their

PT deletion derivatives formed during synthesis

PS Disclosure; Page 79; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the

CC method of the invention. The specification describes a matrix that

CC comprises a support and an affinity unit that specifically and

CC reversibly binds a target oligonucleotide, and comprises a sequence of

CC bases having the reverse complement of a hybridising portion of the

CC target oligonucleotide. The matrix is used for affinity purification of

CC synthetic oligonucleotides, specifically antisense agents, for treatment

CC of hyperproliferative diseases, for treating a non-pathogen,

CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating

CC expression of cell surface proteins, and to inhibit a eukaryotic

CC pathogen, retrovirus or other viruses.

SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

QY 4 tctaccgcgtgcg 17
|||||

Db 1 tctaccgcgtgcg 14

RESULT 13

AAV28174
ID AAV28174 standard; DNA; 17 BP.

AC AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

XX 18-DEC-1997; 97WO-US23284.
PF
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
XX WPI; 1998-362922/31.
DR
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS
SQ Disclosure; Page 80; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX

SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 tctaccgcgtgcg 17
|||||
Db 1 tctaccgcgtgcg 14

RESULT 14
AAV28176
ID AAV28176 standard; DNA; 17 BP.
XX
AC AAV28176;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
XX Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
XX WO9827425-A1.
XX
XX 25-JUN-1998.
PD
XX 18-DEC-1997; 97WO-US23284.
PF
XX 19-DEC-1996; 96US-0769951.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Chen D, Cole DL, Srivatsa GS;
PI
XX WPI; 1998-362922/31.
DR
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

XX
PS Disclosure; Page 82; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX

SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgt 14
|||||
Db 4 cctctaccgcgt 17

RESULT 15
AAV23688
ID AAV23688 standard; DNA; 17 BP.
XX
AC AAV23688;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 141.
XX

KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
PD
XX 01-SEP-1998; 98WO-US18084.
PF
XX 02-SEP-1997; 97US-0923771.
PR

XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
PI
XX WPI; 1999-205198/17.
DR
XX
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.

XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical

CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.

XX
SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccttcctaccgcgt 14
|||||
Db 4 ccttcctaccgcgt 17

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Job time: 8090 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:47 ; Search time 334.55 seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-11

Perfect score: 17

Sequence: 1 cctctaccgcgctgcg 17

Scoring table: IDENTITY NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-465-485A-11
2	17	100.0	17	3	US-09-080-285-11
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4	14	82.4	17	2	US-08-465-485A-12
5	14	82.4	17	3	US-09-080-285-10
6	14	82.4	17	3	US-09-080-285-12
7	12.2	71.8	37	3	US-09-403-267-23
8	11.8	69.4	24	3	US-08-744-550-1
9	11.8	69.4	24	3	US-09-160-671-1
10	11.8	69.4	26	4	US-09-094-557-19
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12	11.8	69.4	28	4	US-09-094-557-26
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15	11.4	67.1	28	4	US-08-870-930-57
16	11.4	67.1	29	4	US-08-870-930-74
17	11.4	67.1	29	4	US-08-870-930-75
18	11.4	67.1	29	4	US-08-870-930-76
19	11.4	67.1	29	4	US-08-870-930-77
20	11.4	67.1	30	4	US-08-870-930-55
21	11.4	67.1	61	4	US-08-870-930-17
22	11.4	67.1	61	4	US-08-870-930-22
23	11.4	67.1	61	4	US-08-870-930-22
24	11.2	65.9	61	4	US-09-275-850-56
25	11.2	65.9	22	3	US-08-526-136-33
26	11.2	65.9	24	5	PCT-US93-06404-1
27	11.2	65.9	28	2	US-08-859-998-111

28	11.2	65.9	28	4	US-09-225-928-111	Sequence 111, App
29	11.2	65.9	33	5	PCT-US95-04583-2	Sequence 2, Appl
30	11.2	65.9	45	2	US-08-450-905B-38	Sequence 38, Appl
31	11.2	65.9	45	3	US-07-982-759F-38	Sequence 38, Appl
32	11.2	65.9	60	1	US-08-484-192-154	Sequence 154, App
33	11	64.7	17	2	US-08-465-485A-9	Sequence 9, Appl
34	11	64.7	17	2	US-08-465-485A-13	Sequence 13, Appl
35	11	64.7	17	3	US-09-080-285-13	Sequence 13, Appl
36	11	64.7	17	3	US-09-080-285-13	Sequence 13, Appl
37	11	64.7	18	4	US-09-030-701-28	Sequence 28, Appl
38	11	64.7	18	4	US-09-286-098-60	Sequence 60, Appl
39	11	64.7	18	4	US-08-960-774-60	Sequence 60, Appl
40	11	64.7	23	4	US-08-870-930-58	Sequence 58, Appl
41	11	64.7	23	4	US-08-870-930-84	Sequence 84, Appl
42	11	64.7	57	3	US-09-135-639-7	Sequence 7, Appl
43	11	64.7	57	3	US-09-135-639-9	Sequence 9, Appl
44	10.8	63.5	15	1	US-08-291-932A-329	Sequence 329, App
45	10.8	63.5	18	3	US-09-199-859-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-11
Sequence 11, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-11

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctgctg 17
|||||
DB 1 CCTTCTACCGCGTGG 17

RESULT 2

US-09-080-285-11
; Sequence 11, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-11

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctgctg 17
|||||
DB 1 CCTTCTACCGCGTGG 17

RESULT 3
US-08-465-485A-10
; Sequence 10, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2075
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-10

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctctaccgctgctg 17
|||||
DB 1 TCCTACCGCGTGG 14

RESULT 4
US-08-465-485A-12
; Sequence 12, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,

US-08-465-485A-12

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-12

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccttcctaccgct 14
Db 4 CCTTCTACCGCGT 17

RESULT 5
US-09-080-285-10
Sequence 10, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-10

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tcttcaccgctgctg 17
Db 1 TCCTACCGCGTGGC 14

RESULT 6
US-09-080-285-12
Sequence 12, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/840,716
;; FILING DATE: 21-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/288,692
;; FILING DATE: 22-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fortney, Andrew D.
;; REGISTRATION NUMBER: 34,600
;; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (408) 436-2070
;; TELEFAX: (408) 436-2075
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
;; US-09-080-285-12

Query Match      82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccttcctaccgcgt 14
    ||| ||| ||| ||| |||
Db 4 CCTTCCTACCGCGT 17

RESULT 7
US-09-403-267-23
; Sequence 23, Application US/09403267
; Patent No. 6159710
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy, and Biology
; APPLICANT: Fraser, Nigel W.
; APPLICANT: Zabolotny, Janice M.
; APPLICANT: Krummenacher, Claude F.
; TITLE OF INVENTION: Method and Compositions for Stabilizing
; TITLE OF INVENTION: Unstable Gene Transcripts
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/403,267
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,664
; FILING DATE: 18-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST8APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
```

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;; LENGTH: 37 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "probe/primer PFPB8"
;; US-09-403-267-23

Query Match      71.8%; Score 12.2; DB 3; Length 37;
Best Local Similarity 82.4%; Pred. No. 44+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ccttcctaccgcgtg 17
    ||| ||| ||| ||| |||
Db 6 CCTTCCTACCGCGCGC 22

RESULT 8
US-08-744-590-1
; Sequence 1, Application US/08744590
; Patent No. 6074823
; GENERAL INFORMATION:
; APPLICANT: Koster, Hubert
; TITLE OF INVENTION: DNA Sequencing By Mass Spectrometry Via
; TITLE OF INVENTION: Exonuclease Degradation
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,590
; FILING DATE: No. 6074823ember 6, 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/388,171
; FILING DATE: February 10, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/034,738
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: SCI-005CNCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-744-590-1

Query Match      69.4%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ccttcctaccgcgtg 15
    ||| ||| ||| ||| |||
Db 3 CATTCCTACCGCGGTG 17
```

RESULT 9
US-09-160-671-1
; Sequence 1, Application US/09160671
; Patent No. 6140053
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY VIA
; TITLE OF INVENTION: EXONUCLEASE DEGRADATION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Edman White & McAlliff
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,671
; FILING DATE: 25-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,272,744,590
; FILING DATE: 10-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/034,738
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2005B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-450-8499
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-160-671-1

Query Match 69.4%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccttcctaccgctg 15
1 ||||| |||||
Db 3 CATTCACCGCGCTG 17

RESULT 10
US-09-094-557-19/c
; Sequence 19, Application US/09094557
; Patent No. 6225531
; GENERAL INFORMATION:
; APPLICANT: Kakitani, Makoto
; APPLICANT: Umemoto, Naoyuki
; APPLICANT: Ishida, Isao
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Yoshikawa, Masaaki

APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-19

Query Match 69.4%; Score 11.8; DB 4; Length 26;
Best Local Similarity 86.7%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cttcctaccgctgc 16
||||| |||||
Db 26 CTTCCACCGCGCTG 12

RESULT 11
US-09-094-557-21
; Sequence 21, Application US/09094557
; Patent No. 6225531
; GENERAL INFORMATION:
; APPLICANT: Kakitani, Makoto
; APPLICANT: Umemoto, Naoyuki
; APPLICANT: Ishida, Isao
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH

TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-21

Query Match 69.4%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgcgtgc 16
|||||
DB 11 CTCTCTACCCCATGC 25

RESULT 12
US-09-094-557-26
Sequence 26, Application US/09094557
Patent No. 6225531
GENERAL INFORMATION:
APPLICANT: Kakitani, Makoto
APPLICANT: Umemoto, Naoyuki
APPLICANT: Ishida, Isao
APPLICANT: Iwamatsu, Akihito
APPLICANT: Yoshikawa, Masaaki
APPLICANT: Yamaoaka, Naoto
TITLE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-26

Query Match 69.4%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgcgtgc 16
|||||
DB 11 CTCTCTACCCCATGC 25

RESULT 13
US-08-185-949B-85
Sequence 85, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-185-949B-85

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 2; Length 66;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ttctctaccgctgcg 17
||||| ||||| |||
Db 14 ttctctaccgctgcg 28

RESULT 14
US-08-870-930-56/c
Sequence 56, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA

FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
US-08-870-930-56

Query Match
Best Local Similarity 67.1%; Score 11.4; DB 4; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctctctaccgct 14
||||| ||||| |
Db 17 ctctctaccgcat 5

RESULT 15
US-08-870-930-57/c
Sequence 57, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: C in position 28 is 2'-OH C
US-08-870-930-57

Query Match
Best Local Similarity 67.1%; Score 11.4; DB 4; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctctctaccgct 14
||||| ||||| |
Db 16 ctctctaccgcat 4

Search completed: June 28, 2002, 22:16:48
Job Time: 8274 sec

Mon Jul 1 08:40:46 2002

us-09-709-170a-11.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:09 ; Search time 3762.88 Seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170a-12
Perfect score: 17
Sequence: 1 gaccctctactccgcgt 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Match Length	ID	Description
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1	17	100.0	17	6	AR052614	AR052614 Sequence
2	14	82.4	17	6	AR052613	AR052613 Sequence
3	14	82.4	17	6	AR052615	AR052615 Sequence
4	12.4	72.9	40	6	AR050327	AR050327 Sequence
5	12.4	72.9	47	9	HUMTCCVJ32	HUMTCCVJ32
6	12.4	72.9	52	9	S63038	S63038
7	12.2	71.8	51	6	AX204129	AX204129
8	12.2	71.8	51	6	AX081385	AX081385
9	12	70.6	47	9	HUMTCCVJ1BQ	HUMTCCVJ1BQ
10	11.8	69.4	21	6	AX012319	AX012319
11	11.8	69.4	25	6	AX022216	AX022216
12	11.8	69.4	25	6	AX030742	AX030742
13	11.8	69.4	25	6	BD008657	BD008657
14	11.8	69.4	30	6	AR125801	AR125801
15	11.8	69.4	30	6	AR125805	AR125805
16	11.8	69.4	30	6	147213	147213
17	11.8	69.4	30	6	147217	147217
18	11.8	69.4	50	6	AX202434	AX202434
19	11.8	69.4	50	6	AX202434	AX202434
20	11.8	69.4	60	10	AF265815	AF265815
21	11.8	69.4	72	9	HUMTCCVJ2B	HUMTCCVJ2B
22	11.4	67.1	18	12	AMM229027	AMM229027
23	11.4	67.1	20	6	BD009422	BD009422
24	11.4	67.1	28	6	AR122834	AR122834
25	11.4	67.1	28	6	AR122835	AR122835
26	11.4	67.1	29	6	AR122852	AR122852
27	11.4	67.1	29	6	AR122853	AR122853
28	11.4	67.1	29	6	AR122854	AR122854
29	11.4	67.1	29	6	AR122855	AR122855
30	11.4	67.1	30	6	AR122833	AR122833
31	11.4	67.1	32	6	AR026317	AR026317
32	11.4	67.1	55	6	AR172872	AR172872
33	11.4	67.1	55	6	AX057560	AX057560
34	11.4	67.1	56	9	HUMTCCVJ1FJ	HUMTCCVJ1FJ
35	11.4	67.1	59	9	HUMTCCVJ2	HUMTCCVJ2
36	11.4	67.1	61	6	AR122795	AR122795
37	11.4	67.1	61	6	AR122800	AR122800
38	11.4	67.1	62	6	AX193276	AX193276
39	11.4	67.1	62	6	AX193441	AX193441
40	11.4	67.1	67	6	AX193327	AX193327
41	11.4	67.1	67	6	AX193345	AX193345
42	11.4	67.1	69	6	AX192906	AX192906
43	11.4	67.1	70	6	AX192919	AX192919
44	11.2	65.9	24	6	AX290793	AX290793
45	11.2	65.9	26	6	A20104	A20104

ALIGNMENTS

RESULT 1						
AR052614	AR052614	17 bp	DNA	linear	PAT 29-SEP-1999	
LOCUS	Sequence 12 from patent US 5831066.					
DEFINITION	AR052614					
ACCESSION	AR052614.1					
VERSION	GI:5975978					
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 17)					
AUTHORS	Reed J.C.					
TITLE	Regulation of bcl-2 gene expression					
JOURNAL	Patent: US 5831066-A 12 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1..17					
	/organism="unknown"					

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Query Match	100.0%;	Score 17;	DB 6;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 56;		

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgct 17
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Db 1 GACCCCTCTACCGCT 17

RESULT 2
AR052613 AR052613 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 11 from patent US 5831066.
ACCESSION AR052613
VERSION AR052613.1 GI:5975977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
JOURNAL Regulation of bcl-2 gene expression
FEATURES Patent: US 5831066-A 11 03-NOV-1998;
Location/Qualifiers
Source 1. .17
/organism="unknown"

BASE COUNT 1 a 8 c 4 g 4 t

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ccttcctaccgct 17
|||||
Db 1 CCTTCTACCGCT 14

RESULT 3
AR052615 AR052615 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 13 from patent US 5831066.
ACCESSION AR052615
VERSION AR052615.1 GI:5975979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
JOURNAL Regulation of bcl-2 gene expression
FEATURES Patent: US 5831066-A 13 03-NOV-1998;
Location/Qualifiers
Source 1. .17
/organism="unknown"

BASE COUNT 3 a 7 c 4 g 3 t

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccg 14
|||||
Db 4 GACCCCTCTACCG 17

RESULT 4
AR050327 AR050327 40 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 17 from patent US 5827684.
ACCESSION AR050327
VERSION AR050327.1 GI:5973052

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Sreekrishna,K., Prevatt,W.D., Thill,G.P., Davis,G.R., Koutz,P.,
Barr,K.A. and Hopkins,S.A.
JOURNAL Production of Bacillus entomotoxins in methylotrophic yeast
FEATURES Patent: US 5827684-A 17 27-OCT-1998;
Location/Qualifiers
Source 1. .40
/organism="unknown"

BASE COUNT 11 a 8 c 10 g 11 t

Query Match 72.9%; Score 12.4; DB 6; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gaccctctaccg 14
|||||
Db 40 GACCCCTCTACCG 27

RESULT 5
HUMTCCVJ32 47 bp mRNA linear PRI 19-AUG-1995
LOCUS
DEFINITION Homo sapiens (C.2.PL252) rearranged T-cell receptor delta chain
(TCRDV2J1) mRNA, partial V-region.
ACCESSION L39499
VERSION L39499.1 GI:945251
KEYWORDS CDR3 region; T-cell receptor alpha-chain; T-cell receptor delta;
antigen recognition site; junctional region; rearranged; variable
region.
SOURCE Homo sapiens (clone: C.2.PL252) colon CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Holtmeier W., Chowers, Y., Lueneng, A., Morzycka-Wroblewska, E. and
Kagnoff, M.F.
JOURNAL The delta T cell receptor repertoire in human colon and peripheral
blood is oligoclonal irrespective of V region usage
MEDLINE J. Clin. Invest. 96 (2), 1108-1117 (1995)
COMMENT Citation paper.
FEATURES Location/Qualifiers
Source 1. .47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C.2.PL252"
/tissue.type="colon"
<1..>47
/gene="TCRDV2J1"
/standard_name="(V delta-2/ J delta-1)"
/note="putative"
1. .47
/gene="TCRDV2J1"
<1..>47
/note="This CDS feature is included to show the
translation of the corresponding V-region. Presently
translation qualifiers on V-region features are illegal."
/codon_start=1
/protein_id="AAC41800.1"
/db_xref="GI:950449"
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BASE COUNT 12 a 6 g 10 t

Query Match 72.9%; Score 12.4; DB 9; Length 47;

Best Local Similarity 92.9%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acccttcctaccgc 15
|||||

Db 10 ACCCTTCTACGAGC 23

RESULT 6

LOCUS S63038 52 bp DNA linear PRI 25-AUG-1993
DEFINITION T cell receptor V delta 1-J delta 1 junction [sample 127] (human,
adult, Genomic, 52 nt).

ACCESSION S63038

VERSION S63038.1 GI:3866400

KEYWORDS

SOURCE

ORGANISM

human adult.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 52)
Beidjord, K., Beidjord, C., Macintyre, E., Even, P. and Sigaux, F.

Peripheral selection of V delta 1+ cells with restricted T cell
receptor delta gene repertoire in the peripheral blood
of healthy donors

J. Exp. Med. 178 (1), 121-127 (1993)

GENBANK 93301568

Genbank staff at the National Library of Medicine created this
entry [NCBI gidsq 134205] from the original journal article.

REMARK This sequence comes from Fig. 2.

FEATURES

source 1..52
/organism="Homo sapiens"

gene 1..52
/partial
/gene="T cell receptor V delta 1-J delta 1 junction"

BASE COUNT 10 a 17 c 11 g 14 t

ORIGIN

Query Match 72.9%; Score 12.4; DB 9; Length 52;
Best Local Similarity 92.9%; Pred. No. 2.6e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccttcctaccgc 17
|||||

Db 20 CCTTCTACGAGC 33

RESULT 7

LOCUS AX204129 51 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 235 from Patent WO0148245.
ACCESSION AX204129

VERSION AX204129.1 GI:15393623

KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)
Shinkens, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof

Patent: WO 0148245-A 235 05-JUL-2001;

JOURNAL Curagen Corporation (US)

FEATURES

source 1..51
/organism="Homo sapiens"

variation /db_xref="taxon:9606"

26 /note="single nucleotide polymorphism"

BASE COUNT 8 a 19 c 16 g 8 t
Accession number cg44036323"

Query Match 71.8%; Score 12.2; DB 6; Length 51;
Best Local Similarity 82.4%; Pred. No. 3.4e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacccttcctaccgc 17
|||||

Db 28 GACCTTCTACGAGC 44

RESULT 8

LOCUS AR081385 67 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 44 from patent US 5972599.
ACCESSION AR081385

VERSION AR081385.1 GI:10008111

KEYWORDS

SOURCE

ORGANISM

Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 67)
Tasset, P., Pagrat, N., Jayasena, S. and Gold, L.

High affinity nucleic acid ligands of cytokines

Patent: US 5972599-A 44 26-OCT-1999;

JOURNAL Location/Qualifiers

FEATURES

source 1..67
/organism="unknown"

BASE COUNT 13 a 13 c 29 g 12 t

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacccttcctaccgc 17
|||||

Db 44 GACCTTCTACGAGC 28

RESULT 9

LOCUS HUMTCVD1BQ 47 bp mRNA linear PRI 10-FEB-1995
DEFINITION Human (clone: 1st1p131) T-cell receptor delta-chain (V-delta-1)
mRNA.

ACCESSION U32414.1 GI:497484

VERSION U32414.1

KEYWORDS T-cell receptor; delta chain.

SOURCE Homo sapiens Intestine cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 47)
Chowers, Y., Holtmeier, W., Harwood, J., Morzycka-Wroblewska, E. and

Kagnoff, M.F.

The V delta 1 T cell receptor repertoire in human small intestine
and colon

J. Exp. Med. 180 (1), 183-190 (1994)

JOURNAL 94275371

FEATURES

source 1..47
/organism="Homo sapiens"

variation /db_xref="taxon:9606"

10 a 15 c 12 g 10 t

BASE COUNT 10 a 15 c 12 g 10 t

ORIGIN

Query Match 70.6%; Score 12; DB 9; Length 47;

Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctctac 12
|||||
Db 9 GACCTTCTCTAC 20

RESULT 10
AX012319/c 21 bp DNA linear PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 7 from Patent WO9553316.
ACCESSION AX012319
VERSION AX012319.1 GI:9998368
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Wiese,M.
TITLE Kinase obtained from leishmania
JOURNAL Patent: WO 955316-A 7 04-NOV-1999;
MAX PLANCK GESELLSCHAFT (DE); WIESE MARTIN (DE)

FEATURES
source 1..21
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR-Primer"

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Best Local Similarity 86.7%; Pred. No. 6.3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 cccctctaccgcgt 17
|||||
Db 17 CCTTCGACCCCGT 3

RESULT 11
AX022216/c 25 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 23 from Patent EP0950098.
ACCESSION AX022216
VERSION AX022216.1 GI:10045876
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: EP 0950098-A 23 20-OCT-1999;
COMM SCIENT IND RES ORG (AU)
FEATURES
source 1..25
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 5 c 13 g 4 t
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Best Local Similarity 86.7%; Pred. No. 6.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 17 ACCCTTACACCGCG 3

RESULT 12
AX030742/c 25 bp DNA linear PAT 20-SEP-2000
LOCUS
DEFINITION Sequence 23 from Patent WO9818918.
ACCESSION AX030742
VERSION AX030742.1 GI:10278250
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: WO 9818918-A 23 07-MAY-1998;
RAMSHAW JOHN ALAN MAURICE (AU); GALANIS MARIA (AU); COMM SCIENT
IND RES ORG (AU); VAUGHAN PAUL RICHARD (AU); WERKMEISTER JEROME
ANTHONY (AU)

FEATURES
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 5 c 13 g 4 t
ORIGIN

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Best Local Similarity 86.7%; Pred. No. 6.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctaccgcg 16
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Db 17 ACCCTTACACCGCG 3

RESULT 13
BD008657/c 25 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Stable expression of the triple helical protein.
ACCESSION BD008657
VERSION BD008657.1 GI:18637030
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Stable expression of the triple helical protein
JOURNAL Patent: JP 2001502548-A 17 27-FEB-2001;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
COMMENT OS Unidentified
PN JP 2001502548-A/17
PD 27-FEB-2001
PF 29-OCT-1997 JP 1998519817
PR PAUL RICHARD VAUGHAN,MARIA GALANIS,JOHN ALAN MAURICE RAMSHAW,
PI JEROME ANTHONY WERKMEISTER
PC C12N15/12,C12N15/81,C12N15/53,C07K14/78,A61K38/39 CC
Strandedness: Single;
CC Topology: Linear;
FH key
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 17 ACCCTTACACCCGCG 3

RESULT 14
 ARI25801/c 30 bp DNA linear PAT 16-MAY-2001
 LOCUS ARI25801
 DEFINITION Sequence 143 from patent US 6177557.
 ACCESSION ARI25801
 VERSION ARI25801.1 GI:14111863
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Janjic,N., Gold,L. and Tasset,D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin
 JOURNAL Patent: US 6177557-A 143 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..30
 /organism="unknown"
 BASE COUNT 5 a 4 c 17 g 4 t
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Query Match 69.4%; Score 11.8; DB 6; Length 30;
 Best Local Similarity 86.7%; Pred. No. 6.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 27 ACCCATCTACCCCG 13

RESULT 15
 ARI25805/c 30 bp DNA linear PAT 16-MAY-2001
 LOCUS ARI25805
 DEFINITION Sequence 147 from patent US 6177557.
 ACCESSION ARI25805
 VERSION ARI25805.1 GI:14111867
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

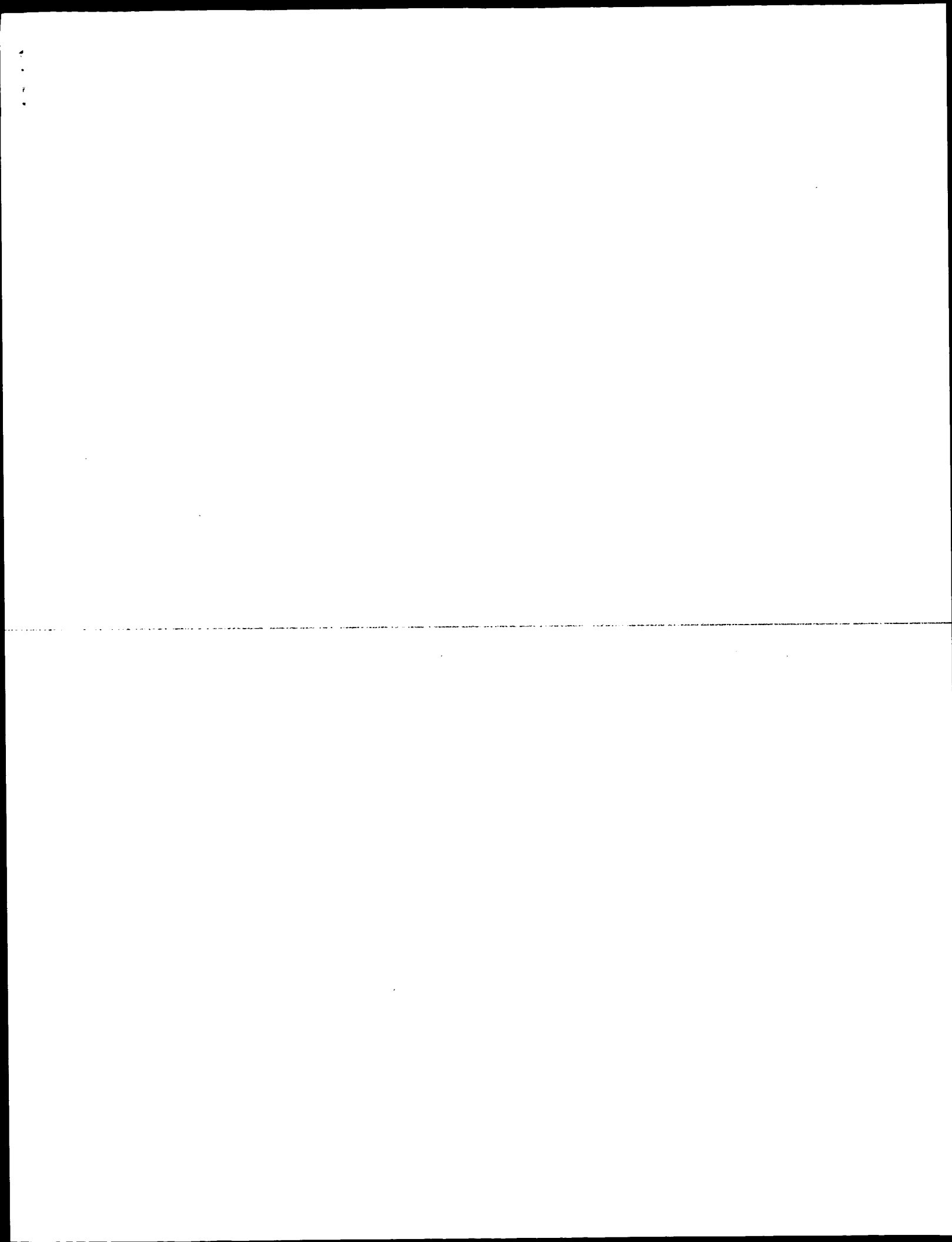
REFERENCE 1 (bases 1 to 30)
 AUTHORS Janjic,N., Gold,L. and Tasset,D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin
 JOURNAL Patent: US 6177557-A 147 23-JAN-2001;
 FEATURES Location/Qualifiers
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BASE COUNT 5 a 4 c 17 g 4 t
 ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 30;
 Best Local Similarity 86.7%; Pred. No. 6.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctcctaccgcg 16
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 Db 27 ACCCATCTACCCCG 13

Search completed: June 28, 2002, 22:11:11
 Job time: 8362 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:14 ; Search time 1381.16 Seconds
(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170A-12

Perfect score: 17

Sequence: 1 gaccctctaccgcgt 17

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_032802:*

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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	16	AA086654
2	17	100.0	17	19	AAV28176
3	17	100.0	17	20	AAV23688
4	17	100.0	17	20	AAV18697
5	15	88.2	20	16	AA086643
6	15	88.2	20	19	AAV28169
7	15	88.2	20	20	AAV23681
8	15	88.2	20	20	AAV18690
9	15	88.2	20	21	AAV29348

10	14	82.4	17	16	AA086653	Bcl-2 antisense ol
11	14	82.4	17	16	AA086655	Bcl-2 antisense ol
12	14	82.4	17	19	AAV28175	Antisense oligonuc
13	14	82.4	17	19	AAV28177	Antisense oligonuc
14	14	82.4	17	20	AAV23687	Deletion sequence
15	14	82.4	17	20	AAV23689	Deletion sequence
16	14	82.4	17	20	AAV18696	Target bcl-2 antis
17	14	82.4	17	20	AAV18698	Target bcl-2 antis
18	14	82.4	19	17	AAV27370	Anti-ras oncogene
19	12.2	71.8	27	19	AAV63985	Mycobacterium tube
20	12.2	71.8	27	20	AAV81049	PCR primer for clo
21	12.2	71.8	37	18	AAV87143	IFN-gamma 2'NH2 RN
22	12.2	71.8	51	22	AAV79620	Human DNA containi
23	11.8	69.4	17	21	AAV02633	Hammerhead ribozym
24	11.8	69.4	17	21	AAV02634	Hammerhead ribozym
25	11.8	69.4	21	21	AAV24128	L. mexicana lmpk p
26	11.8	69.4	25	19	AAV27135	Synthetic human co
27	11.8	69.4	30	16	AAV27135	Two member family
28	11.8	69.4	30	16	AAV27135	bFGF 2'-NH2 RNA II
29	11.8	69.4	30	21	AAV3304	Arabidopsis acyltr
30	11.8	69.4	30	22	AAV37460	2'NH2 RNA ligand t
31	11.8	69.4	30	22	AAV70681	2'NH2 RNA ligand t
32	11.8	69.4	40	21	AAV70685	Polynucleotide seq
33	11.8	69.4	50	22	AAV26153	Non-target oligo N
34	11.8	69.4	50	22	AAV11596	Non-target oligo N
35	11.4	67.1	20	19	AAV73521	H. pylori vacA pri
36	11.4	67.1	20	20	AAV05149	PCR primer used to
37	11.4	67.1	32	20	AAV5589	Primer for Ngp II
38	11.4	67.1	36	21	AAV3739	Permutin linker e
39	11.4	67.1	51	22	AAV32896	Human SNP oligonuc
40	11.4	67.1	55	22	AAV81393	Rat GLUT4/myc epit
41	11.4	67.1	61	21	AAV69861	VEGF-binding nucle
42	11.4	67.1	62	22	AAV29289	Colon tumour relat
43	11.4	67.1	62	22	AAV29454	Colon tumour relat
44	11.4	67.1	67	22	AAV29340	Colon tumour relat
45	11.4	67.1	67	22	AAV29358	Colon tumour relat

ALIGNMENTS

RESULT 1	
AA086654	AA086654 standard; DNA; 17 BP.
XX	XX
AC	AA086654:
XX	XX
DT	27-SEP-1995 (first entry)
XX	XX
DE	Bcl-2 antisense oligonucleotide.
XX	XX
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	XX
OS	Synthetic.
XX	XX
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..17
FT	/tag= a
XX	/note= "3'-5' (antisense) sequence"
XX	XX
PN	WO9508350-A.
XX	XX
PD	30-MAR-1995.
XX	XX
PF	20-SEP-1994; 94WO-US10725.
XX	XX
PR	20-SEP-1993; 93US-0124256.
XX	XX
PA	(REED/) REED J C.
XX	XX
PI	Reed JC.
XX	XX

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX Example 12; Page 33; 108pp; English.
XX Antisense oligonucleotides were tested for their ability to induce
CC antisense cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccctctaccgcgt 17
1 | | | | | | | | | | | | | | | | | | | |
Db 1 gaccctctaccgcgt 17

RESULT 2
AAV28176
ID AAV28176 standard; DNA; 17 BP.
XX
XX AAV28176;
XX
XX 08-OCT-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
DE
XX Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
XX Synthetic.
OS
XX WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI; 1998-362922/31.
XX
XX Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX
XX Disclosure; Page 82; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccctctaccgcgt 17
1 | | | | | | | | | | | | | | | | | | | |
Db 1 gaccctctaccgcgt 17

RESULT 3
AAV23688
ID AAV23688 standard; DNA; 17 BP.
XX
XX AAV23688;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 141.
DE
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.
XX
XX Synthetic.
OS
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX
XX WPI; 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23546-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccgcgt 17
|||||
Db 1 gacccttctaccgcgt 17

RESULT 4

AAV28169 standard; DNA; 17 BP.

AAV28169;

10-MAY-1999 (first entry)

Target bcl-2 antisense oligonucleotide #29.

Cellular adhesion protein; proliferation; antisense oligonucleotide;
alimentary canal; transport; gastrointestinal mucosa; cancer;
Alzheimer's disease; beta-thalassemia; malaria; viral infection;
HIV; inflammation; ss.

Synthetic.

WO9901579-A1.

14-JAN-1999.

01-JUL-1998; 98WO-US13574.

01-JUL-1997; 97US-0886829.

(ISIS-) ISIS PHARM INC.

Hardee G, Teng C;

WPI: 1999-106077/09.

Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability

Example 2; Page 85; 11pp; English.

A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAV28169 to AAV28179 and AAV28180 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccgcgt 17
|||||
Db 1 gacccttctaccgcgt 17

RESULT 5

AAQ86643 standard; DNA; 20 BP.

AAQ86643;

27-SEP-1995 (first entry)

Antisense oligomer TI-AS.

Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
ss.

Synthetic.

Location/Qualifiers

Key 1.20
FT misc_feature
FT /tag- a
FT /note- "3'-5' (antisense) sequence"

WO9508350-A.

30-MAR-1995.

20-SEP-1994; 94WO-US10725.

20-SEP-1993; 93US-0124256.

(REED/) REED J C.

Reed JC;

WPI: 1995-139394/18.

Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer

Disclosure; Page 13; 10pp; English.

The antisense oligonucleotide TI-AS straddles the translation-initiation site in the mRNA coding strand of the human bcl-2 gene and is complementary to this region. It reduces the expression of bcl-2 gene product thereby inducing programmed cell death of certain cancer cells.

Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 83; Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 cccttctaccgcgt 17
|||||
Db 1 cccttctaccgcgt 15

RESULT 6

AAV28169 standard; DNA; 20 BP.

AAV28169;

08-OCT-1998 (first entry)

Antisense oligonucleotide to bcl-2 mRNA.

Purification; oligonucleotide; matrix; affinity unit;
affinity purification; antisense; bcl-2; ss.

Synthetic.

XX WO9827425-A1.
XX 25-JUN-1998.
XX 18-DEC-1997; 97WO-US23284.
XX 19-DEC-1996; 96US-0769951.
XX (ISIS-) ISIS PHARM INC.
XX Chen D, Cole DL, Srivatsa GS;
XX WPI, 1998-362922/31.
XX Matrix for selective separation of oligonucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
XX Disclosure; Page 76; 183pp; English.
XX AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridizing portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, for treating a non-pathogen,
XX non-hyperproliferative disease, e.g. Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 cccctcctaccgcgt 15

RESULT 7
AAAX23681
ID AAX23681 standard; DNA; 20 BP.
XX
XX AAX23681;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 134.
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.
XX
XX Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX

XX WPI, 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX
XX Example 9; Page 147; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
XX sensor arrays, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion sequence
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labeled and
XX hybridize with the probe oligonucleotides of the sensor arrays. Such
XX oligonucleotides and their targets are represented in AAX23548-X23709.
XX Oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion or
XX proliferation, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
XX Syncytial Virus or cytomegalovirus (CMV). The compositions enable
XX characterization of deletion sequence oligonucleotides having related,
XX but different nucleobase sequences, and quantification of different
XX species of deletion sequence ("target") oligonucleotides in a mixture.
XX Also, if the specificity of the oligonucleotide's nucleobase sequence
XX for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 cccctcctaccgcgt 15

RESULT 8
AAX18690
ID AAX18690 standard; DNA; 20 BP.
XX
XX AAX18690;
XX
XX 10-MAY-1999 (first entry)
XX
XX Target bcl-2 antisense oligonucleotide #22.
XX
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
XX alimentary canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection;
XX HIV; inflammation; ss.
XX
XX Synthetic.
XX
XX WO9901579-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13574.
XX
XX 01-JUL-1997; 97US-0886829.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Hardee G, Teng C;
XX
XX WPI, 1999-106077/09.
XX
XX

PT Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability

PS Example 2; Page 83; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35,%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AA418669 to AA418799 and AA418801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.

SO Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 cccctctaccgcgt 17

Db 1 cccctctaccgcgt 15

RESULT 9

AA49348

ID AA49348 standard; DNA; 20 BP.

AC AA49348;

DT 14-MAR-2000 (first entry)

DE bcl-2 targeted antisense oligonucleotide SEQ ID 13.

KW Cellular proliferation; expression; modulation; antisense;

KW non-parenteral; delivery; uptake; administration; emulsion;

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;

ss.

OS Synthetic.

OS Homo sapiens.

PN WO960012-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US11394.

PR 21-MAY-1998; 98US-0082624.

PA (ISIS-) ISIS PHARM INC.

PI Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

DR WPI: 2000-072428/06.

PT New oligonucleotide compositions used for the non-parenteral delivery
 PT of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular
 PT decoys, external guide sequences or aptamers
 XX Example 2; Page 122; 133pp; English.

CC Sequences AA49344-249354, AA49384-249385, AA49387-249388 and

CC AA49392-24993 represent antisense oligonucleotides designed

CC to modulate the rate of cellular proliferation. The invention relates to

CC new compositions for the non-parenteral delivery of oligonucleotides

CC comprising at least one oligonucleotide in an emulsion. Oligonucleotides

CC delivered via the compositions of the invention can be used to modulate

CC expression of a cellular adhesion protein, modulate a rate of cellular

CC proliferation, or have biological activity against eukaryotic pathogens

CC or retroviruses. They can be used for treating conditions including

CC e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease

CC or undue cellular proliferation. The compositions can enhance the local

CC and systemic uptake and delivery of nucleic acids via non-parenteral

CC routes of administration (e.g., via the alimentary canal, skin, eyes,

CC pulmonary tract, urethra or vagina).

SO Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 cccctctaccgcgt 17

Db 1 cccctctaccgcgt 15

RESULT 10

AA086653

ID AA086653 standard; DNA; 17 BP.

AC AA086653;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

KW Anticancer oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss.

OS Synthetic.

Location/Qualifiers

Key misc_feature /tag="a"

note="3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

XX Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS1846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA086650-55) or the 5'-cap
 CC region (AA086656-58) of human bcl-2 pre-mRNA.

SO Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ccttcctaccgct 17
 |||||
 DB 1 ccttcctaccgct 14

RESULT 11

AAQ86655 standard; DNA; 17 BP.

AC AAQ86655;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KM Anticore oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 lymphoma; programmed cell death, ss.

OS Synthetic.

FT Key Location/Qualifiers
 FT misc-feature 1..17
 /tag= a
 /note= "3'-5' (antisense) sequence"

W09508350-A.

30-MAR-1995.

PE 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumors, esp. breast cancer
 XX

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targets
 CC against the translation initiation site (AAQ86650-55) or the 5'-cap
 CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.

XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccttcctaccg 14
 |||||
 DB 4 gaccttcctaccg 17

RESULT 12

AAV28175 standard; DNA; 17 BP.

AC AAV28175;

XX 08-OCT-1998 (first entry)

XX Antisense oligonucleotide to bcl-2 mRNA.

DE Purification; oligonucleotide; matrix; affinity unit;

KM affinity purification; antisense; bcl-2; ss.

XX Synthetic.

PN W09827425-A1.

XX 25-JUN-1998.

PD 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

XX Chen D, Cole DL, Srivatsa GS;

PI WPI; 1998-362922/31.

XX Matrix for selective separation of oligonucleotide - useful for,
 PT e.g. large scale purification of anti-sense agents from their
 PT deletion derivatives formed during synthesis

PS Disclosure; Page 81; 183pp; English.

XX AAV28155-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridizing portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.

XX Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ccttcctaccgct 17
 |||||
 DB 1 ccttcctaccgct 14

RESULT 13

AAV28177 standard; DNA; 17 BP.

AC AAV28177;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KM Purification; oligonucleotide; matrix; affinity unit;

KM affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN W09827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 83; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcg 14
Db 4 gaccctctaccgcg 17

RESULT 14
AA23687
ID AAX23687 standard; DNA; 17 BP.
XX
AC AAX23687;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 140.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target

PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.
PS
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cctctaccgcgcgt 17
Db 1 cctctaccgcgcgt 14

RESULT 15
AA23689
ID AAX23689 standard; DNA; 17 BP.
XX
AC AAX23689;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 142.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 151; 163pp; English.

XX This invention describes a novel composition comprising a number of
 CC sensor arrays, where each array comprises a unique probe
 CC oligonucleotide, which is the reverse complement of part of a unique
 CC target oligonucleotide present in a mixture of target deletion sequence
 CC oligonucleotides. The compositions form a method for characterizing a
 CC sample of target deletion oligonucleotides which are labeled and
 CC hybridize with the probe oligonucleotides of the sensor arrays. Such
 CC oligonucleotides and their targets are represented in AAX23548-X23709.
 CC Oligonucleotides characterized by the method form pharmaceutical
 CC compositions that are useful for modulating cellular adhesion or
 CC proliferation, and being active against a eukaryotic pathogen, a human
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
 CC characterization of deletion sequence oligonucleotides having related,
 CC but different nucleobase sequences, and quantification of different
 CC species of deletion sequence ("target") oligonucleotides in a mixture.
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence
 CC for its reverse complement is not modified, the method may be performed
 CC using oligodeoxynucleotides.

XX
 SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccg 14
 |||||
 Db 4 gacccttctaccg 17

Search completed: June 28, 2002, 22:40:15
 Job time: 8091 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:48 ; Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-12

Perfect score: 17

Sequence: 1 gacccctcaccgcgt 17

Scoring table: IDENTITY NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCNUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-465-485A-12
2	17	100.0	17	3	US-09-080-285-12
3	14	82.4	17	2	US-08-465-485A-11
4	14	82.4	17	2	US-08-465-485A-13
5	14	82.4	17	3	US-09-080-285-13
6	14	82.4	17	3	US-09-080-285-13
7	12.4	72.9	40	1	US-08-231-342-17
8	12.2	71.8	67	2	US-08-477-527A-44
9	12.2	71.8	67	3	US-08-481-710-44
10	12.2	71.8	67	5	PCT-US96-0937-44
11	11.8	69.4	30	1	US-08-384-708A-143
12	11.8	69.4	30	1	US-08-384-708A-147
13	11.8	69.4	30	4	US-08-687-421-143
14	11.8	69.4	30	4	US-08-687-421-147
15	11.4	67.1	28	4	US-08-870-930-56
16	11.4	67.1	28	4	US-08-870-930-57
17	11.4	67.1	29	4	US-08-870-930-74
18	11.4	67.1	29	4	US-08-870-930-75
19	11.4	67.1	29	4	US-08-870-930-76
20	11.4	67.1	29	4	US-08-870-930-77
21	11.4	67.1	30	4	US-08-870-930-55
22	11.4	67.1	32	2	US-08-305-764C-21
23	11.4	67.1	55	4	US-08-531-025-5
24	11.4	67.1	61	4	US-08-870-930-17
25	11.4	67.1	61	4	US-08-870-930-22
26	11.4	67.1	61	4	US-09-275-850-56
27	11.2	65.9	26	1	US-08-318-193-28

28	11.2	65.9	26	1	US-08-318-193-29	Sequence 29, Appl
29	11.2	65.9	30	1	US-08-236-311-14	Sequence 14, Appl
30	11.2	65.9	50	3	US-08-457-918-14	Sequence 14, Appl
31	11.2	65.9	52	6	5200327-11	Patent No. 5200327
32	11.2	65.9	60	1	US-08-484-192-154	Sequence 154, App
33	11.2	65.9	70	2	US-08-894-578-138	Sequence 138, App
34	11	64.7	17	2	US-08-465-485A-10	Sequence 10, Appl
35	11	64.7	17	3	US-09-080-285-10	Sequence 10, Appl
36	11	64.7	23	4	US-08-870-930-58	Sequence 10, Appl
37	11	64.7	23	4	US-08-870-930-84	Sequence 84, Appl
38	11	64.7	57	3	US-09-135-639-9	Sequence 9, Appl
39	11	64.7	57	3	US-09-135-639-7	Sequence 9, Appl
40	11	64.7	60	4	US-09-339-913B-26	Sequence 26, Appl
41	11	64.7	60	4	US-09-339-904A-26	Sequence 26, Appl
42	11	64.7	60	4	US-08-769-062B-26	Sequence 26, Appl
43	11	64.7	60	4	US-09-344-002B-26	Sequence 26, Appl
44	10.8	63.5	24	3	US-08-744-590-1	Sequence 1, Appl
45	10.8	63.5	24	3	US-09-160-671-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-12
Sequence 12, Application US/08465485A
Patent No. 3631066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-12

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
|||||
DB 1 GACCTTCTACCGCGT 17

RESULT 2

US-09-080-285-12
; Sequence 12, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-09-080-285-12

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
|||||
DB 1 GACCTTCTACCGCGT 17

RESULT 3
US-08-465-485A-11
; Sequence 11, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-465-485A-11

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cctctaccgcgt 17
|||||
DB 1 CCTTCTACCGCGT 14

RESULT 4
US-08-465-485A-13
; Sequence 13, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

US-08-465-485A-13
; Sequence 13, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-13

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 1 gacccttctaccg 14
DB 4 GACCCTCTCTACCG 17

RESULT 5
US-09-080-285-11
Sequence 11, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-11

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 4 ccttcctaccgct 17
DB 1 CCTTCCTACCGCT 14

RESULT 6
US-09-080-285-13
Sequence 13, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-13

Query Match
Best Local Similarity 82.4%; Score 14; DB 3; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaccctctaccg 14
|||||
Db 4 GACCCCTCTACCG 17

RESULT 7
US-08-231-342-17/c
Sequence 17, Application US/08231342
Patent No. 5827684
GENERAL INFORMATION:
APPLICANT: Sreekishna, Kotikanyadanam
APPLICANT: Prevalat, William D
APPLICANT: Thill, Gregory P
APPLICANT: Davila, Geneva R
APPLICANT: Koutz, Patricia
APPLICANT: Barr, Kathryn A
APPLICANT: Hopkins, Sharon A
TITLE OF INVENTION: Production of Bacillus Entomotoxins in
TITLE OF INVENTION: Methyloctrophic Yeast
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. Lasalle St.
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603-4277
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,342
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,448
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REGISTRATION NUMBER: 33,129
REFERENCE/DOCKET NUMBER: 52627
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842

TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-231-342-17

Query Match
Best Local Similarity 72.9%; Score 12.4; DB 1; Length 40;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gaccctctaccg 14
|||||
Db 40 GACCCCTCTACCG 27

RESULT 8
US-08-477-527A-44/c
Sequence 44, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-477-527A-44

Query Match 71.8%; Score 12.2; DB 2; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
||||| || |||||
DB 44 GACCCTTACTCTCGCGT 28

RESULT 9
US-08-481-710-44/C
Sequence 44, Application US/08481710
Patent No. 6028186
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,710
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
APPLICATION DATA:
APPLICATION NUMBER: 07/114,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearen
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-44

Query Match 71.8%; Score 12.2; DB 3; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
||||| || |||||
DB 44 GACCCTTACTCTCGCGT 28

RESULT 10
PCT-US96-09537-44/C
Sequence 44, Application PC/TUS9609537
GENERAL INFORMATION:
APPLICANT: NEXSTAR PHARMACEUTICALS, INC.
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09537
FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/481,710
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX41/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-44

Query Match 71.8%; Score 12.2; DB 5; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 gacccttctaccgcgt 17
||||| 11 |||||
Db 44 GACCTTACTCTCGCGT 28

RESULT 11
US-08-384-708A-143/c

; Sequence 143, Application US/08384708A
; Patent No. 5639868

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

; TITLE OF INVENTION: Fibroblast Growth Factors

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,708A

; FILING DATE: 02-FEBRUARY-1995

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/195,005

; FILING DATE: 10-FEBRUARY-1994

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX07/D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 143:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: All C's are 2'-NH2 cytosine

; OTHER INFORMATION: All U's are 2'-NH2 uracil

; US-08-384-708A-143

Query Match 69.4%; Score 11.8; DB 1; Length 30;

Best Local Similarity 86.7%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 acccttctaccgcg 16
||||| 11 |||||
Db 27 ACCCATCTACCCCG 13

RESULT 12

US-08-384-708A-147/c
; Sequence 147, Application US/08384708A
; Patent No. 5639868

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

; TITLE OF INVENTION: Fibroblast Growth Factors

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,708A

; FILING DATE: 02-FEBRUARY-1995

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/195,005

; FILING DATE: 10-FEBRUARY-1994

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX07/D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 147:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: All C's are 2'-NH2 cytosine

; OTHER INFORMATION: All U's are 2'-NH2 uracil

; US-08-384-708A-147

Query Match 69.4%; Score 11.8; DB 1; Length 30;

Best Local Similarity 86.7%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 acccttctaccgcg 16
||||| 11 |||||
Db 27 ACCCATCTACCCCG 13

RESULT 13

US-08-687-421-143/c

; Sequence 143, Application US/08687421

; Patent No. 6177557

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

; TITLE OF INVENTION: Fibroblast Growth Factors

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,708A

; FILING DATE: 02-FEBRUARY-1995

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/195,005

; FILING DATE: 10-FEBRUARY-1994

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX07/D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 147:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: All C's are 2'-NH2 cytosine

; OTHER INFORMATION: All U's are 2'-NH2 uracil

; US-08-687-421-143/c

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-687-421-143

Query Match 69.4%; Score 11.8; DB 4; Length 30;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctacgcgcg 16
||||| ||||| |||
DB 27 ACCCATCTACCCCG 13

RESULT 14
US-08-687-421-147/C
Sequence 147, Application US/08687421
Patent No. 6177557
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa

APPLICANT: Tassel, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-687-421-147

Query Match 69.4%; Score 11.8; DB 4; Length 30;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctacgcgcg 16
||||| ||||| |||
DB 27 ACCCATCTACCCCG 13

RESULT 15
US-08-870-930-56/C
Sequence 56, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:

APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
US-08-870-930-56

Query Match 67.1%; Score 11.4; DB 4; Length 28;
Best Local Similarity 92.3%; Pred. No. 8.5e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 cttctaccgcgt 17
|||||||
Db 17 CTTCTACGCGCAT 5

Search completed: June 28, 2002, 22:16:49
Job time: 8275 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:11 ; Search time 3762.88 Seconds

(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-13

Perfect score: 17

Sequence: 1 ggagaccctctctaccg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues 794432

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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1	17	100.0	17	6	AR052615	AR052615 Sequence
2	14	82.4	17	6	AR052614	AR052614 Sequence
3	13.8	81.2	72	9	HUMTCGDB	M28772 Human T-cell
4	13.4	78.8	47	9	HUMTCVD1BQ	I32414 Human T-cell
5	12.8	75.3	45	6	A50066	A50066 Sequence 18
6	12.8	75.3	45	6	AR083363	AR083363 Sequence
7	12.8	75.3	47	9	HUMTCVJ32	I39499 Homo sapien
8	12.8	75.3	51	6	AX204517	AX204517 Sequence
9	12.4	72.9	18	6	AX119389	AX119389 Sequence
10	12.4	72.9	20	6	BD009422	BD009422 Probes, m
11	12.4	72.9	40	6	AR050327	AR050327 Sequence
12	12.2	71.8	53	9	HUMTCVD1DN	I32463 Human T-cell
13	12.2	71.8	59	9	HUMTCRAD2	I39615 Homo sapien
14	12.2	71.8	71	6	AR092263	AR092263 Sequence
15	12	70.6	60	6	AR172707	AR172707 Sequence
16	11.8	69.4	18	6	A52768	A52768 Sequence 12
17	11.8	69.4	18	6	AR137982	AR137982 Sequence
18	11.8	69.4	18	6	AX138682	AX138682 Sequence
19	11.8	69.4	19	6	AR097399	AR097399 Sequence
20	11.8	69.4	19	6	I25704	I25704 Sequence 23
21	11.8	69.4	60	6	AR068207	AR068207 Sequence
22	11.8	69.4	60	6	AR076959	AR076959 Sequence
23	11.8	69.4	60	6	AR078792	AR078792 Sequence
24	11.8	69.4	71	6	I05090	I05090 Sequence 1
25	11.8	69.4	74	6	AR147504	AR147504 Sequence
26	11.4	67.1	18	6	AX098738	AX098738 Sequence
27	11.4	67.1	20	6	E03458	E03458 Oligo DNA P
28	11.4	67.1	20	6	E03451	E03451 Oligonucleo
29	11.4	67.1	26	6	AR089980	AR089980 Sequence
30	11.4	67.1	28	6	AX283122	AX283122 Sequence
31	11.4	67.1	28	6	AX283124	AX283124 Sequence
32	11.4	67.1	32	6	AR026317	AR026317 Sequence
33	11.4	67.1	48	6	AX201571	AX201571 Sequence
34	11.4	67.1	50	6	AX164949	AX164949 Sequence
35	11.4	67.1	51	6	AX204129	AX204129 Sequence
36	11.4	67.1	51	6	AX204257	AX204257 Sequence
37	11.4	67.1	55	6	AR172872	AR172872 Sequence
38	11.4	67.1	55	6	AX057560	AX057560 Sequence
39	11.4	67.1	60	10	AF265815	AF265815 Mus muscu
40	11.4	67.1	62	6	AX193276	AX193276 Sequence
41	11.4	67.1	62	6	AX193441	AX193441 Sequence
42	11.4	67.1	67	6	AX193327	AX193327 Sequence
43	11.4	67.1	67	6	AX193345	AX193345 Sequence
44	11.4	67.1	68	6	AX1650	AX1650 Sequence 7
45	11.4	67.1	68	6	A73712	A73712 Sequence 5

ALIGNMENTS

RESULT 1
LOCUS AR052615 17 bp DNA
DEFINITION Sequence 13 from patent US 5831066.
ACCESSION AR052615
VERSION AR052615.1 GI:5975979
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 13 03-NOV-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 3 a 7 c 4 g 3 t
ORIGIN

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacccttctaccg 17
Db 1 GGAGACCTTCTCTACCG 17

RESULT 2

AR052614

LOCUS AR052614 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5831066.
ACCESSION AR052614
VERSION AR052614.1 GI:5975978
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 12 03-NOV-1998;
FEATURES
Source location/Qualifiers
1.17
/organism="unknown"

BASE COUNT 2 a 8 c 3 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gacccttctaccg 17
Db 1 GACCTTCTCTACCG 14

RESULT 3

HMTGCD2B

LOCUS HMTGCD2B 72 bp DNA linear PRI 03-AUG-1993
DEFINITION Human T-cell receptor trans-rearranged gamma-delta-chain gene
V-gamma-D-delta-J-delta region, clone gd2.2.
ACCESSION M28772.1 GI:339093
VERSION M28772
KEYWORDS
D-region: J-region; N-region; T-cell receptor; T-cell receptor
delta chain; T-cell receptor gamma chain; V-region; antigen
receptor; processed gene.
SOURCE Human thymus DNA, clone gd2.2.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Tycko, B., Palmer, J. and Sklar, J.
TITLE T cell receptor gene trans-rearrangements: Chimeric gamma-delta
genes in normal lymphoid tissues
JOURNAL Science 245, 1242-1246 (1998)
MEDLINE 89388234
FEATURES
Source location/Qualifiers
1.72
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="T-cell receptor gamma-delta-chain V-D-J-region"

CDS

/codon_start=3
/protein_id="AAA36693.1"
/db_xref="GI:353708"
/translation="CATWEPPTARGMFCYDKLIFGK"
BASE COUNT 15 a 20 c 18 g 19 t
ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 72;
Best Local Similarity 88.2%; Pred. No. 2.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagacccttctaccg 17
Db 14 GGAGACCTTCTCTACTG 30

RESULT 4

HMTGCD1BQ

LOCUS HMTGCD1BQ 47 bp mRNA linear PRI 10-FEB-1995
DEFINITION Human (clone: 1st1p131) T-cell receptor delta-chain (V-delta-1)
mRNA.
ACCESSION L32414
VERSION L32414.1 GI:497484
KEYWORDS T-cell receptor; delta chain.
SOURCE Homo sapiens intestine cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Chowers, Y., Holtmeier, W., Harwood, J., Morzycka-Wroblewska, E. and
Kagnoff, M.F.
TITLE The V delta 1 T cell receptor repertoire in human small intestine
and colon
JOURNAL J. Exp. Med. 180 (1), 183-190 (1994)
MEDLINE 94275371
FEATURES
Source location/Qualifiers
1.47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="intestine"

BASE COUNT 10 a 15 c 12 g 10 t
ORIGIN

Query Match 78.8%; Score 13.4; DB 9; Length 47;
Best Local Similarity 93.3%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagacccttctaccg 15
Db 6 GGAGACCTTCTCTAC 20

RESULT 5

A50066

LOCUS A50066 45 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 18 from Patent WO9612810.
ACCESSION A50066
VERSION A50066.1 GI:2303244
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Lathe, R., Rose, K.A. and Stapleton, G.
TITLE HIPPOCAMPUS-ASSOCIATED PROTEINS, DNA SEQUENCES CODING THEREFOR AND
USUS THEREFOR
JOURNAL Patent: WO 9612810-A 18 02-MAY-1996;
UNIV EDINBURGH (GB)
COMMENT Other publication AU 3670395 960515.
FEATURES
Source location/Qualifiers
1.45
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 12 a 15 c 5 g 13 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 45;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctacc 16
|||||
Db 22 GGAGTCCCTCTACC 37

RESULT 6
AR083363 45 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 17 from patent US 5976850.
ACCESSION AR083363
VERSION AR083363.1 GI:10010153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Lathé, R., Rose, R., Andrew and Stapleton, G.
TITLE Hippocampus-associated proteins; DNA sequences coding therefor and uses thereof
JOURNAL Patent: US 5976850-A 17 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..45
/organism="unknown"
BASE COUNT 12 a 15 c 5 g 13 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 45;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ggagaccctctacc 16
|||||
Db 22 GGAGTCCCTCTACC 37

RESULT 7
HMTCCVJ32 47 bp mRNA linear PRI 19-AUG-1995
LOCUS Homo sapiens (C.2.PL252) rearranged T-cell receptor delta chain
DEFINITION (TCRDVJ32) mRNA, partial V-region.
ACCESSION L39499
VERSION L39499.1 GI:945251
KEYWORDS CD3 region; T-cell receptor alpha-chain; T-cell receptor delta; antigen recognition site; junctional region; rearranged; variable region.
SOURCE Homo sapiens (clone: C.2.PL252) colon cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Holtmeier, W., Chowers, Y., Lumeng, A., Morzycka-Wroblewska, E. and Kagnoff, M.F.
TITLE The delta T cell receptor repertoire in human colon and peripheral blood is oligoclonal irrespective of V region usage
JOURNAL J. Clin. Invest. 96 (2), 1108-1117 (1995)
MEDLINE 95362812
COMMENT Citation paper.
FEATURES Location/Qualifiers
source 1..47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C.2.PL252"
/tissue_type="colon"
/feature="V-region"

gene
CDS
/gene="TCRDVJ32"
/note="This CDS feature is included to show the location/Qualifiers"

translation of the corresponding V-region. Presently translation qualifiers on V-region features are illegal."
/codon_start=1
/protein_id="AAC41800.1"
/db_xref="GI:950449"
/translation="ACDRLPTALPNAYKL"
BASE COUNT 12 a 19 c 6 g 10 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 9; Length 47;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ggagaccctctaccg 17
|||||
Db 7 GACACCTCTCTACAG 22

RESULT 8
AX204517 51 bp DNA linear PAT 30-AUG-2001
LOCUS Sequence 623 from Patent WO0148245.
DEFINITION AX204517
ACCESSION AX204517
VERSION AX204517.1 GI:15394084
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0148245-A 623 05-JUL-2001;
CURRAT Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism
Accession number c943970982"

BASE COUNT 13 a 14 c 17 g 7 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ggagaccctctacc 16
|||||
Db 25 GGAGACCTGCTTACC 40

RESULT 9
AX119389 18 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 46 from Patent WO0129251.
DEFINITION AX119389
ACCESSION AX119389
VERSION AX119389.1 GI:14036308
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Messiaen, L. and Callens, T.
TITLE Improved mutation analysis of the nfi gene
JOURNAL Patent: WO 0129251-A 46 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers

source 1.18
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 6 c 3 g 6 t

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagagacctccta 14
||| ||||| |||||
Db 4 GGAGACCTCTCCTA 17

RESULT 10
BD009422 20 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples.
ACCESSION BD009422
VERSION BD009422.1 GI:18637795
KEYWORDS JP 2001502536-A/14.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Quint,W. and Doorn,L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 14 27-FEB-2001;
COMMENT INNOGENETICS NV,DDL BV
OS Unidentified
PN JP 2001502536-A/14
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C1201/68,C07K14/205,C12M15/11
CC
FH
FT source 1.20
Location/Qualifiers
/organism="Unidentified".

FEATURES
source 1.20
Location/Qualifiers
/organism="Unidentified"
/db_xref="taxon:32644"

BASE COUNT 4 a 8 c 3 g 4 t 1 others

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.8e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagagacctcctacg 17
||| ||||| |||||
Db 4 GARACCGTCTCTACG 19

RESULT 11
AR050327 40 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 17 from patent US 5827684.
ACCESSION AR050327
VERSION AR050327.1 GI:5973052
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Steekrisma,K., Prevatt,W.D., Thill,G.P., Davis,G.R., Koutz,P.,

TITLE Barr,K.A. and Hopkins,S.A.
JOURNAL Production of Bacillus entomotoxins in methylotrophic yeast
Patent: US 5827684-A 17 27-OCT-1998;
FEATURES Location/Qualifiers
source 1.40
/organism="Unknown"

BASE COUNT 11 a 8 c 10 g 11 t

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 40;
Best Local Similarity 92.9%; Pred. No. 1.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gacctctctacg 17
||| ||||| |||||
Db 40 GACCGTCTCTACG 27

RESULT 12
HUMTCVD1DN 53 bp mRNA linear PRI 10-FEB-1995
LOCUS
DEFINITION Human (clone: 3cpj23) T-cell receptor delta-chain (V-delta-1) mRNA.
ACCESSION L32463
VERSION L32463.1 GI:497533
KEYWORDS T-cell receptor; delta chain.
SOURCE Homo sapiens intestine cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 53)
AUTHORS Chowers,Y., Holtmeier,W., Harwood,J., Morzycka-Wroblewska,E. and
Kagnoff,M.F.
TITLE The V delta 1 T cell receptor repertoire in human small intestine
and colon
JOURNAL J. Exp. Med. 180 (1), 183-190 (1994)
MEDLINE 94275371
FEATURES Location/Qualifiers
source 1.53
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="intestine"

BASE COUNT 7 a 15 c 18 g 13 t

ORIGIN

Query Match 71.8%; Score 12.2; DB 9; Length 53;
Best Local Similarity 82.4%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gagagacctcctacg 17
||| ||||| |||||
Db 6 GGAGACCTCTCTACTG 22

RESULT 13
HUMTCRAD2 59 bp mRNA linear PRI 21-AUG-1995
LOCUS
DEFINITION Homo sapiens (C.A.LR02) rearranged T-cell receptor delta chain
(TCRAVL452-TCRDJ1) mRNA, partial V-region.
ACCESSION L39615
VERSION L39615.1 GI:945298
KEYWORDS CDR3 region; T-cell receptor alpha-chain; T-cell receptor delta;
antigen recognition site; junctional region; rearranged; variable
region.
SOURCE Homo sapiens (clone: C.A.LR02) colon cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 59)
AUTHORS Holtmeier,W., Chowers,Y., Lumeng,A., Morzycka-Wroblewska,E. and
Kagnoff,M.F.
TITLE The delta T cell receptor repertoire in human colon and peripheral

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us-09-709-170a-13.szlm75.rge

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagaccctctaccg 17
Db 1 ggagaccctctaccg 17
|||||
1 ggagaccctctaccg 17

RESULT 2
AAV28177
ID AAV28177 standard; DNA: 17 BP.
XX
AC AAV28177;
XX
DT 08-OCF-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KW Purification: oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 83; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagaccctctaccg 17
Db 1 ggagaccctctaccg 17
|||||
1 ggagaccctctaccg 17

RESULT 3
AAV23689
ID AAV23689 standard; DNA: 17 BP.
XX
AC AAV23689;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 142.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 96WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 151; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using Oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacccctctaccg 17
|||||
Db 1 ggagacccctctaccg 17

RESULT 4

AAAX18698
ID AAX18698 standard; DNA; 17 BP.

AC AAX18698;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #30.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KM Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KX HIV; inflammation; ss.

XX Synthetic.

OS WO9901579-A1.

PN 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13574.

XX 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

XX Hardee G, Teng C;

XX WPI; 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used

PT particularly for delivering therapeutic antisense oligonucleotides

PS across the gastrointestinal mucosa, provides high bioavailability

XX Example 2: Page 85; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a

CC nucleic acid and at least one penetration enhancer. The compositions are

CC used: (i) to treat or prevent any disease or disorder that can be

CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,

CC beta-thalassemia, malaria, viral infections (including human immune

CC deficiency virus (HIV), inflammation, in human or animal medicine;

CC (ii) to investigate the role of a gene or gene product in non-human

CC animals; and (iii) to modulate gene expression in cells, tissues or

CC organs. The compositions provide bioavailability of at least 15,

CC preferably 17-35,%. The penetration enhancer improves: (i) transport of

CC the nucleic acid across the mucosa of the alimentary canal and into

CC cells; and (ii) increases stability of the nucleic acid. Oral

CC administration avoids the complications and expense of intravenous or

CC other methods of administration. AAX18699 to AAX18799 and AAX18801

CC represent antisense oligonucleotides which can be used as the nucleic

CC acid in the method of the invention.

CC Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

SO

RESULT 5

AAQ86654
ID AAQ86654 standard; DNA; 17 BP.

AC AAQ86654;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.

XX Synthetic.

OS Key Location/Qualifiers

FT 1..17 /tag- a

FT misc-feature /note- "3'-5' (antisense) sequence"

XX WO9508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US10725.

XX 20-SEP-1993; 93US-0124256.

XX (REED/) REED J C.

XX Reed JC;

XX WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce

CC programmed cell death (DNA fragmentation) in the human lymphoma cell

CC line RS1846. The oligonucleotides are phosphodiester targeted

CC against the translation initiation site (AAQ86650-55) or the 5'-cap

CC region (AAQ86656-58) of human bcl-2 pre-mRNA.

XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

SO

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gacccctctaccg 17
|||||

Db 1 gacccctctaccg 14

RESULT 6

AAV28176
ID AAV28176 standard; DNA; 17 BP.

AC AAV28176;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

XX Purification: oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

KX Synthetic.

OS

PN WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI: 1998-362922/31.
XX
XX Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX Disclosure; Page 82; 183pp; English.
XX
XX AAX28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 gaccctctaccg 17
| | | | | | | | | | | | | | | | | |
DB 1 gaccctctaccg 14

RESULT 7
AAX23688
ID AAX23688 standard; DNA; 17 BP.
XX
XX AAX23688;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 141.
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
XX Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX

DR WPI: 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 gaccctctaccg 17
| | | | | | | | | | | | | | | | | |
DB 1 gaccctctaccg 14

RESULT 8
AAX18697
ID AAX18697 standard; DNA; 17 BP.
XX
XX AAX18697;
XX
XX 10-MAY-1999 (first entry)
XX
XX Target bcl-2 antisense oligonucleotide #29.
XX
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
KW alimentary canal; transport; gastrointestinal mucosa; cancer;
KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW HIV; inflammation; ss.
XX
XX Synthetic.
XX
XX WO9901579-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13574.
XX
XX 01-JUL-1997; 97US-0886829.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Hardee G, Teng C;
XX
XX WPI: 1999-106077/09.
XX
XX Composition comprising nucleic acid and penetration enhancer - used
PT

PT particularly for delivering therapeutic antisense oligonucleotides
PR across the gastrointestinal mucosa, provides high bioavailability
XX
PS Example 2; Page 85; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAX18669 to AAX18799 and AAX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX
SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gacacctctaccg 17
|||||
DB 1 gacacctctaccg 14

RESULT 9

AAFO2633
ID AAF02633 standard; DNA; 17 BP.

XX AAF02633;

AC 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #928.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KM interferon alpha, ss.

XX Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US09721.

PR 12-APR-1999; 99US-0129390.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, McSwiggen J;

DR WPI; 2000-647423/62.

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
protein, interferon alpha and erythropoietin -

PS Claim 37; Page 77; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CATT Displacement

CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.

XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 75.3%; Score 12.8; DB 21; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagacctctaccg 17
|||||
DB 1 gagacctctaccg 16

RESULT 10

AAT29732
ID AAT29732 standard; DNA; 45 BP.

XX AAT29732;

DE 16-AUG-1996 (first entry)

XX Rat clone 13 Hct-1 probe.

XX Hippocampus-associated protein; Hct-1; cytochrome-P450;

KW steroid transformation; neuropsychiatric disorder; cognition;
KM neurodegenerative disease; endocrine disorder; diagnosis;

XX probe, ss.

OS Synthetic.

PN WO9612810-A1.

PD 02-MAY-1996.

PF 18-OCT-1995; 95WO-GB02465.

PR 19-OCT-1994; 94GB-0021093.

XX (UYED-) UNIV EDINBURGH.

PI Lathe R, Rose KA, Stapleton G;

DR WPI; 1996-230611/23.

XX Novel hippocampus-associated proteins, Hct-1 - related to
PT cytochrome(s) P450 and useful for catalytic transformation of
PT substrates

PS Disclosure; Page 28; 70pp; English.

CC A synthetic DNA probe (AAT29732) is based on a rat Hct-1 cDNA
CC clone (see also AAT29723), beginning 112 nt 5' from the polyA tail.
CC It can be used with a rat Hct-1 probe (AAT29729) and Mathans mouse
CC Hct-1 (AAT29730) for in situ hybridizations to detect Hct-1 in
CC brain tissue.

XX
SQ Sequence 45 BP; 12 A; 15 C; 5 G; 13 T; 0 other;

Query Match 75.3%; Score 12.8; DB 17; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gagacctctaccg 16
|||||
DB 22 gagacctctaccg 37

RESULT 11

AAH80008
ID AAH80008 standard; DNA: 51 BP.
AC AAH80008;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 623.
XX
KM Human: single nucleotide polymorphism: SNP: angiotensin;
KM 4-hydroxybutyrate; dehydrogenase; protein therapy;
KM adenosine triphosphate-dependent RNA helicase;
KM major histocompatibility complex Class I histocompatibility antigen; MHC;
KM phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KM antineumatic; antisclerotic; antidiabetic; antineoplastic; cytosolic;
KM antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200148245-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US53346.
XX
PR 27-DEC-1999; 99US-0472688.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-418297/44.
XX
PT Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections -
XX
PS Claim 1; Page 240; 484pp; English.
XX
CC The invention relates to nucleic acids (AAH93386-AAH80036) encoding
CC polymorphic variants of proteins (AAH98010-AAH98238) related to
CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antineumatic, antisclerotic, antidiabetic, antineoplastic, cytosolic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC major histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC the nervous system, an infection of pathogenic organisms. They may also
CC be used to alter phenotypic traits such as longevity, appearance,
CC strength, speed and endurance.
XX
SQ Sequence 51 BP; 13 A; 14 C; 17 G; 7 T; 0 other;

Query Match 75.3%; Score 12.8; DB 22; Length 51;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctacc 16
IIIIIIIIIIIIIIII
DB 25 ggagaccctggtacc 40

RESULT 12
AAS04946
ID AAS04946 standard; DNA: 18 BP.
XX
AC AAS04946;
XX
DT 07-SEP-2001 (first entry)
XX
DE Neurofibromatosis (NF1) cDNA sequencing primer #31.
XX
KM Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
KM Epstein-Barr virus; B-lymphoblastoid cell; phytohemagglutinin; PHA;
KM frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
KM sequencing primer.
XX
OS Homo sapiens.
XX
PN WO200129251-A2.
XX
PD 26-APR-2001.
XX
PF 18-OCT-2000; 2000WO-EP10255.
XX
PR 18-OCT-1999; 99EP-0870216.
PR 05-JUN-2000; 2000EP-0870122.
PR 16-JUN-2000; 2000US-0211629.
XX
PA (UYGE-) UNIV GENT.
XX
PI Messiaen L, Callens T;
XX
DR WPI: 2001-300341/31.
XX
PT Mutation analysis of NF1 gene by treating EBV transformed
PT lymphoblastoid cell lines formed with lymphocytes of patient with
PT protein synthesis inhibitor, and obtaining peptides by translating
PT amplified RNA from cell line -
XX
PS Claim 9; Page 57; 102pp; English.
XX
CC The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing
CC Epstein-Barr virus (EBV) transformed B-lymphoblastoid cell line with
CC stimulation, or short-term culturing of PBL by phytohemagglutinin (PHA)
CC isolated PBL, or short-term culturing of the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which the
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity, by using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts.
XX
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 other;

Query Match 72.9%; Score 12.4; DB 22; Length 18;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagaccctctcta 14
IIIIIIIIIIIIIIII
DB 4 ggtgaccctctcta 17

RESULT 13

AAV73521
ID AAV73521 standard; DNA: 20 BP.
XX
XX AAV73521;
XX
XX 22-MAR-2000 (first entry)
XX
XX H. pylori vacA primer VALXR.
XX
XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDg;
XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
XX
XX Helicobacter pylori.
XX
XX MO9816658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997; 97WO-EP05614.
XX
XX 16-OCT-1996; 96EP-0870131.
XX 09-SEP-1997; 97EP-0870133.
XX
XX (INNO-) INNOGENETICS NV.
XX (DDL-) DDL BV.
XX
XX Quint W, Van Doorn L;
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains
XX comprises use of primers and probes based on vacA and cagA gene
XX
XX Claim 2; Page 44; 122pp; English.
XX
XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX virulence determinant genes (VDg) e.g. the cytotoxin-associated (cagA)
XX gene. The method allows the typing and allele-specific detection of a
XX strain according to the VDg alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements
XX involved in enabling, determining, and marking the infectivity and/or
XX pathogenicity of the H. pylori strain. The method provides a way of
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
XX determining eradication therapy. AAV73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX The primers and probes are used especially to detect the vacA S regions
XX S1a/b/c and S2 and the M regions M1 and M2 which are represented in
XX AAV73547-V73785.
XX
XX Sequence 20 BP; 4 A; 8 C; 3 G; 4 T; 1 other;

Query Match 72.9%; Score 12.4; DB 19; Length 20;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagacccctctaccg 17
11:111 111111111
Db 4 garaccgtctctacag 19

RESULT 14

AAZ26082/c

AAZ26082 standard; DNA: 21 BP.

AAZ26082;

30-NOV-1999 (first entry)

Human polymorphic region 271.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.

OS Homo sapiens.

PN WO9841648-A2.

PD 24-SEP-1998.

PE 19-MAR-1998; 98WO-US05419.

PR 20-MAR-1997; 97US-0041057.

PA (VAR-) VARIAGENICS INC.

PI Housman D, Ledley FD, Stanton VP;

DR WPI: 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for
XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
XX plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
XX Disclosure; Figure 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is
XX active on a gene vital for cell growth or viability, and where the gene
XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can
XX be used in the diagnosis, prevention and treatment of LOH disorders,
XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney
XX disease, and graft versus host disease. The method can also be used to
XX remove malignant cells from bone marrow transplants. AAZ25812-226825
XX represent human polymorphic sites described in the method of the
XX invention.

XX Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 other;

Query Match 72.9%; Score 12.4; DB 19; Length 21;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gagacccctctacc 15
111 111111111
Db 15 GAGGCCCTTCTAC 2

RESULT 15

AA011413/c
ID AA011413 standard; DNA: 17 BP.
XX

AC AAD11413;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Plasmid B1154 disruption cassette amplifying PCR primer OSCXKS14.
 XX
 KW Five-carbon sugar; aldo-sugar; keto-sugar; sugar alcohol; fermentation;
 KW pentose phosphate pathway; xylitol; D-arabitol; D-arabinose; D-lyxose;
 KW ribitol; D-ribose; D-ribulose; D-xylose; D-xylulose; microbial host;
 KW arabitol phosphate dehydrogenase; APDH; xylitol phosphate dehydrogenase;
 KW APDH; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200153306-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-JAN-2001; 2001WO-FI00051.
 XX
 PR 21-JAN-2000; 2000US-0488581.
 XX
 PA (XYRO-) XYROFIN OY.
 XX
 PI Miasnikov A, Ojamo H, Povelainen M, Gros H, Toivari M, Richard P;
 PI Ruohonen L, Kolivrantia K, Londresborough J, Aristidou A;
 PI Penttilae M, Plazancet-Menut C, Deutscher J;
 XX
 DR WPI; 2001-465360/50.
 XX
 PT Isolated polynucleotide, used to transform bacterial or yeast hosts
 PT which can then be used in the production of sugars and sugar alcohols,
 PT encodes xylitol phosphate dehydrogenase -
 XX
 PS Example 12; Page 188; 205pp; English.
 XX
 CC The present invention relates to the methods for manufacturing
 CC five-carbon aldo- and keto-sugars and sugar alcohols by fermentation in
 CC recombinant hosts. The recombinant hosts of the invention have been
 CC engineered to enhance the production of the pentose phosphate pathway
 CC intermediates, or the production of one or more of xylitol, D-arabitol,
 CC D-arabinose, D-lyxose, ribitol, D-ribose, D-ribulose, D-xylose and/or
 CC D-xylulose. Arabitol phosphate dehydrogenase (APDH) is used in a
 CC microbial host cell to produce recombinant arabitol. Xylitol phosphate
 CC dehydrogenase (XPDH) and arabitol phosphate dehydrogenase are used in a
 CC microbial host cell to produce recombinant xylitol. The present sequence
 CC is a PCR primer which is used for the amplification of disruption
 CC cassette of plasmid B1154, used in the exemplification of the invention.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 other;

Query Match 71.88; Score 12.2; DB 22; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ggagaccctcctacgg 17
 ||||| ||||| ||
 Db 17 GGAGATCCTTCTTAGCG 1

Search completed: June 28, 2002, 22:40:16
 Job time: 8092 sec

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:49 : Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-13

Perfect score: 17
Sequence: 1 ggaagaccctctctacg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	2	US-08-465-485A-13 Sequence 13, Appl
2	17	100.0	17	3	US-09-080-285-13 Sequence 13, Appl
3	14	82.4	17	2	US-08-465-485A-12 Sequence 12, Appl
4	14	82.4	17	3	US-09-080-285-12 Sequence 12, Appl
5	12.8	75.3	45	2	US-08-845-161A-17 Sequence 17, Appl
6	12.8	75.3	45	4	US-09-270-751-17 Sequence 17, Appl
7	12.4	72.9	40	1	US-08-231-342-17 Sequence 17, Appl
8	12.2	71.8	71	2	US-08-894-578-201 Sequence 201, App
9	12	70.6	60	4	US-09-339-913B-26 Sequence 26, Appl
10	12	70.6	60	4	US-09-339-904A-26 Sequence 26, Appl
11	12	70.6	60	4	US-08-769-062B-26 Sequence 26, Appl
12	12	70.6	60	4	US-09-344-002B-26 Sequence 26, Appl
13	11.8	69.4	18	3	US-08-894-173-12 Sequence 12, Appl
14	11.8	69.4	18	4	US-09-398-193-12 Sequence 12, Appl
15	11.8	69.4	19	1	US-08-388-381-23 Sequence 23, Appl
16	11.8	69.4	19	5	US-08-765-626-23 Sequence 23, Appl
17	11.8	69.4	19	5	PCT-US95-08605-23 Sequence 23, Appl
18	11.8	69.4	60	2	US-08-663-566A-40 Sequence 40, Appl
19	11.8	69.4	60	2	US-08-023-610-40 Sequence 40, Appl
20	11.8	69.4	60	2	US-08-288-065A-40 Sequence 40, Appl
21	11.8	69.4	60	2	US-08-362-240A-40 Sequence 40, Appl
22	11.8	69.4	60	5	PCN-US95-10245-40 Sequence 40, Appl
23	11.8	69.4	74	4	US-09-315-793-14 Sequence 14, Appl
24	11.4	67.1	20	3	US-09-418-641-82 Sequence 82, Appl
25	11.4	67.1	26	2	US-08-859-998-100 Sequence 100, App
26	11.4	67.1	26	4	US-09-225-928-100 Sequence 100, App
27	11.4	67.1	32	2	US-08-305-764C-21 Sequence 21, Appl

ALIGNMENTS

28	11.4	67.1	55	4	US-09-591-025-5	Sequence 5, Appl1
29	11.4	67.1	70	4	US-09-025-769B-129	Sequence 129, App
30	11.2	65.9	19	3	US-09-290-449-11	Sequence 11, Appl
31	11.2	65.9	24	1	US-08-116-389-23	Sequence 23, Appl
32	11.2	65.9	24	1	US-08-708-431-23	Sequence 23, Appl
33	11.2	65.9	24	2	US-08-880-830-23	Sequence 23, Appl
34	11.2	65.9	24	5	PCT-US94-13895-23	Sequence 23, Appl
35	11.2	65.9	25	1	US-08-276-919-11	Sequence 11, Appl
36	11.2	65.9	25	1	US-08-776-088-16	Sequence 16, Appl
37	11.2	65.9	25	5	PCT-US95-09145A-16	Sequence 16, Appl
38	11.2	65.9	27	1	US-08-116-389-22	Sequence 22, Appl
39	11.2	65.9	27	1	US-08-169-303-6	Sequence 6, Appl1
40	11.2	65.9	27	1	US-08-708-431-22	Sequence 22, Appl
41	11.2	65.9	27	2	US-08-880-830-22	Sequence 22, Appl
42	11.2	65.9	27	2	US-08-791-883-3	Sequence 3, Appl1
43	11.2	65.9	27	3	US-09-023-673-3	Sequence 3, Appl1
44	11.2	65.9	27	5	PCT-US94-13895-22	Sequence 22, Appl
45	11.2	65.9	48	1	US-07-618-946B-17	Sequence 17, Appl

RESULT 1
US-08-465-485A-13
Sequence 13, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
? ANTI-SENSE: YES
US-08-465-485A-13

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacctctctaccg 17
|||||
Db 1 GGAGACCTTCTCTACCG 17

RESULT 2

US-09-080-285-13
; Sequence 13, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-09-080-285-13

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacctctctaccg 17
|||||
Db 1 GGAGACCTTCTCTACCG 17

RESULT 3

US-08-465-485A-12
; Sequence 12, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-465-485A-12

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gacctctctaccg 17
|||||
Db 1 GACCTTCTCTACCG 14

RESULT 4

US-09-080-285-12
; Sequence 12, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-12

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gaccctctacg 17
|||||
Db 1 GACCCTCTACCG 14

RESULT 5
US-08-845-161A-17
Sequence 17, Application US/08845161A
Patent No. 5976850
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS: DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-845-161A-17

Query Match 75.3%; Score 12.8; DB 2; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggaagaccctctacg 16
|||||
Db 22 GGAGTCCCATCTACG 37

RESULT 6
US-09-270-751-17
Sequence 17, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS: DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-270-751-17

Query Match 75.3%; Score 12.8; DB 4; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctacc 16
|||||
Db 22 GGAGTCCCATCTACC 37

RESULT 7
US-08-231-342-17/C
Sequence 17, Application US/08231342
Patent No. 5827684
GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikanadanam
APPLICANT: Prevatt, William D
APPLICANT: Thill, Gregory P
APPLICANT: Davis, Geneva R
APPLICANT: Koutz, Patricia
APPLICANT: Barr, Kathryn A
APPLICANT: Hopkins, Sharon A
TITLE OF INVENTION: Production of Bacillus Entomotoxins in
TITLE OF INVENTION: Methylotrophic Yeast
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603-4277
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,342
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,448
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REGISTRATION NUMBER: 33,129
REFERENCE/DOCKET NUMBER: 52627
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-231-342-17

Query Match 72.9%; Score 12.4; DB 1; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gaccctctaccg 17
|||||
Db 40 GACCGTCCCTACCG 27

RESULT 8
US-08-894-578-201
Sequence 201, Application US/08894578
Patent No. 5998142
GENERAL INFORMATION:
APPLICANT: GOLD et al.
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
TITLE OF INVENTION: BY EXPONENTIAL ENRICHMENT:
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03097
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: 22-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234,997
FILING DATE: 28-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/309,245
FILING DATE: 20-SEPTEMBER-1994
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX28/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs

;; PRIOR FILING DATE: 1996-12-18
;; PRIOR APPLICATION NUMBER: 08/198,431
;; PRIOR FILING DATE: 1994-02-17
;; PRIOR APPLICATION NUMBER: 08/425,684
;; PRIOR FILING DATE: 1995-04-18
;; PRIOR APPLICATION NUMBER: 08/537,874
;; PRIOR FILING DATE: 1995-10-30
;; NUMBER OF SEQ ID NOS: 101
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 26
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: degenerate
;; OTHER INFORMATION: oligonucleotide used for codon usage library
US-09-344-002B-26

Query Match 70.6%; Score 12; DB 4; Length 60;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagaccctcctcctac 16
| :||:||||:|:|:|
Db 20 gargayccctcctcctac 35

RESULT 13
US-08-894-173-12
;; Sequence 12, Application US/08894173A
;; Patent No. 6090612
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; TITLE OF INVENTION: Adenylate cyclase and uses therefor
;; FILE REFERENCE: P14716C
;; CURRENT APPLICATION NUMBER: US/08/894,173A
;; CURRENT FILING DATE: 1997-08-13
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO: 12
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: STRANDEDNESS : Single
;; FEATURE:
;; OTHER INFORMATION: TOPOLOGY : Linear
;; FEATURE:
;; OTHER INFORMATION: MOLECULE TYPE : CDNA
;; FEATURE:
;; OTHER INFORMATION: HYPOTHETICAL : NO
;; FEATURE:
;; OTHER INFORMATION: ANTI-SENSE : YES
;; FEATURE:
;; OTHER INFORMATION: CELL LINE : A1720
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer to
;; OTHER INFORMATION: 1kb extension of cDNA clone jpl34 of A1720
US-08-894-173-12

Query Match 69.4%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctcctcctac 15
||||| |||||
Db 1 ggagagagctcctcctac 15

RESULT 14
US-09-398-193-12

;; Sequence 12, Application US/09398193
;; Patent No. 6197581
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; TITLE OF INVENTION: Adenylate cyclase and uses therefor
;; FILE REFERENCE: P24360-
;; CURRENT APPLICATION NUMBER: US/09/398,193
;; CURRENT FILING DATE: 1999-09-17
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO: 12
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: STRANDEDNESS : Single
;; FEATURE:
;; OTHER INFORMATION: TOPOLOGY : Linear
;; FEATURE:
;; OTHER INFORMATION: MOLECULE TYPE : CDNA
;; FEATURE:
;; OTHER INFORMATION: HYPOTHETICAL : NO
;; FEATURE:
;; OTHER INFORMATION: ANTI-SENSE : YES
;; FEATURE:
;; OTHER INFORMATION: CELL LINE : A1720
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer to
;; OTHER INFORMATION: 1kb extension of cDNA clone jpl34 of A1720
US-09-398-193-12

Query Match 69.4%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctcctcctac 15
||||| |||||
Db 1 ggagagagctcctcctac 15

RESULT 15
US-08-388-381-23/c
;; Sequence 23, Application US/08388381
;; Patent No. 5552283
;; GENERAL INFORMATION:
;; APPLICANT: Diamandis, Eleftherios
;; APPLICANT: Dunn, James M.
;; APPLICANT: Stevens, John K.
;; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
;; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
;; NUMBER OF SEQUENCES: 41
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson
;; STREET: 1992 Commerce Street, Suite 309
;; CITY: Yorktown Heights
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10598-4412
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS 5.0
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/388,381
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/271,946
;; FILING DATE: 08-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marina T. Larson

```

;
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 23:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: sequencing primer for exon 2 of human p53 gene
;
US-08-388-381-23

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Query Match 69.4%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 gagaccttctacc 16
   ||||| ||||| |||
Db 19 GAGACGCTTCCAACC 5

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Search completed: June 28, 2002, 22:16:50
 Job time: 8276 sec

11
12
13
14

	Matches	15; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	gcggcgacagcgcg	15						
Dd	1	gcggcgacagcgcg	15						

RESULT	2			
AX107320				
LOCUS	AX107320	33 bp	DNA	
DEFINITION	Sequence 139 from Patent WO0123606.		linear	PAT 30-APR-2001
ACCESSION	AX107320			
VERSION	AX107320.1	GI:13922805		
KEYWORDS				
SOURCE				
ORGANISM	Pectobacterium chrysanthemi.			
	Pectobacterium chrysanthemi			

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
1 (bases 1 to 33)	Grabowski, R. and Berghof, K.	Nucleic acid molecules for detecting bacteria and phylogenetic units of bacteria	Patent: WO 0123606-A 139 05-APR-2001; Biotecan Diagnostics GmbH (DE)	source 1..33 location/Qualifiers	3 a	11 c 14 g 5 t
				/organism="Pectobacterium chrysanthemi" /db_xref="taxon:556"		

Query Match	89.3%	Score 13.4	DB 6	Length 33
Best Local Similarity	93.3%	Pred. No. 1	1e+05	
Matches 14	Conservative	0	Mismatches 1	Indels 0
Gy	1	gagcgcgacagcgcg	15	
db	6	gcgcgcgtracgcgg	20	

RESULT	3				
LOCUS	AX099682/c				
DEFINITION	AX099682	40 bp	DNA	linear	PAT 02-APR-2001
ACCESSION	Sequence AX099682	38 from Patent WO011976.			
VERSION	AX099682.1	GI:13538736			
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 40)				
AUTHORS	Anderson,H.M., Chay,C.A., Chen,G. and Conner,T.W.				
TITLE	Plant regulatory sequences for control of gene expression				
JOURNAL	Patent: WO 011976-A 38 22-MAR-2001;				
	MONSANTO COMPANY (US).				

source	1. 40			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			
	/note="primer"			
BASE COUNT	3 a	17 c	13 g	7 t
ORIGIN				

	89.3%;	Score 13.4;	DB 6;	length 40;
Query Match				
Best Local Similarity	93.3%;	Pred. No. 1,	le+05;	
Matches 14; conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	1 ggcggcgccagcggg	15		
Db	26 gccgccgcaccgcgg	12		

RESULT	4	20 bp	DNA	1 linear	PAT 29-SEP-1995
AR052628	AR052628	Sequence	28 from patent US 5831066.		
LOCUS	AR052628	AR052628			
DEFINITION	AR052628	AR052628			
ACCESSION	AR052628	AR052628			
VERSION	AR052628.1	GI:5975992			
KEYWORDS					

REFERENCE	1	(bases 1 to 20)	unclassified.
AUTHORS	Reed, J C.		
TITLE	Regulation of bcl-2 gene expression		
JOURNAL	Patent: US 5831066-A 28 03-NOV-1998		
FEATURES	Location/Qualifiers		
source	1..20		
BASE COUNT	2 a	7 c	11 g
ORIGIN			0 t

Query Match	86.7%;	Score 13;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.9e+05;		
Matches 13;	Conservative	0;	Mismatches 0;	Indels 0;
Qy	1	gagagcagacagc	13	
Db	8	gcgcgcgcacgcc	20	

[illegible]

Query Match	82.7%	Score 12.4	DB 6	Length 20
Best Local Similarity	92.9%	Pred. No. 3.5e+05		
Matches 13; Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY	1	gcgcgcgcacgcgcg	14	
Db	7	GCgcgcgcgcgcgcg	20	

LOCUS	AX146640	RESULT 6
DEFINITION	Sequence 16 from Patent WO034817.	25 bp DNA
ACCESSION	AX146640	linear
VERSION	AX146640.1	PAT 31-MAY-2001
KEYWORDS	GI:14285033	
SOURCE	Zea mays.	
ORGANISM	Zea mays.	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	

REFERENCE 1 (bases 1 to 25)
AUTHORS helent Jaris/T.G.
TITLE Genes encoding enzymes for lignin biosynthesis and uses thereof
JOURNAL Patent: WO 0134817-A 16 17-MAY-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source 1..25
/organism="zea mays"
/db_xref="taxon:4577"
BASE COUNT 4 a 7 c 10 g 4 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cgcgcgacgacg 14
|||||
Db 10 GCGCGCGACGCG 23

RESULT 7
AXI47141 30 bp DNA linear PAT 08-JUN-2001
LOCUS AXI47141
DEFINITION Sequence 99 from Patent WO0136481.
ACCESSION AXI47141
VERSION AXI47141.1 GI:14346317
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 99 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacg 15
|||||
Db 7 CAGCGCGACGCG 20

RESULT 8
AXI47142 30 bp DNA linear PAT 08-JUN-2001
LOCUS AXI47142
DEFINITION Sequence 100 from Patent WO0136481.
ACCESSION AXI47142
VERSION AXI47142.1 GI:14346318
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 100 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacg 15
|||||
Db 24 CAGCGCGACGCG 11

RESULT 9
AXI47155 30 bp DNA linear PAT 08-JUN-2001
LOCUS AXI47155
DEFINITION Sequence 113 from Patent WO0136481.
ACCESSION AXI47155
VERSION AXI47155.1 GI:14346326
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 113 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacg 15
|||||
Db 24 CAGCGCGACGCG 11

RESULT 10
AXI47156 30 bp DNA linear PAT 08-JUN-2001
LOCUS AXI47156
DEFINITION Sequence 114 from Patent WO0136481.
ACCESSION AXI47156
VERSION AXI47156.1 GI:14346327
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 114 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cggcgagcagcgcg 15
1 | | | | | | | | | |
Db 7 CAGCGGCGAGCGCGG 20

RESULT 11
AX147157/c 30 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 115 from Patent WO0136481.
DEFINITION AX147157
ACCESSION AX147157
VERSION AX147157.1 GI:14346328
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 115 25-MAY-2001;
FEATURES location/Qualifiers
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cggcgagcagcgcg 15
1 | | | | | | | | | |
Db 24 CAGCGGCGAGCGCGG 11

RESULT 12
AX147158 30 bp DNA linear PAT 08-JUN-2001
LOCUS AX147158
DEFINITION Sequence 116 from Patent WO0136481.
ACCESSION AX147158
VERSION AX147158.1 GI:14346329
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 116 25-MAY-2001;
FEATURES location/Qualifiers
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT 7 a 15 g 1 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 cggcgagcagcgcg 15
1 | | | | | | | | | |
Db 7 CAGCGGCGAGCGCGG 20

RESULT 13
A91129/c 70 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 8 from Patent WO9827225.
DEFINITION A91129
ACCESSION A91129
VERSION A91129.1 GI:6740159
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 70)
AUTHORS Cardy, D.L.
TITLE ASSAY INVOLVING LOOPED NUCLEIC ACID
JOURNAL Patent: WO 9827225-A 8 25-JUN-1998;
CARDY DONALD LEONARD NICHOLAS (GB); CYTOCELL LTD (GB)
FEATURES location/Qualifiers
source 1..70
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 26 c 26 g 16 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cggcgagcagcgcg 15
1 | | | | | | | | | |
Db 70 CGAGCGGCGAGCGCGG 57

RESULT 14
AR081378 70 bp DNA linear PAT 31-AUG-2000
LOCUS AR081378
DEFINITION Sequence 37 from patent US 5972599.
ACCESSION AR081378
VERSION AR081378.1 GI:10008104
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 70)
AUTHORS Tasset, D., Pagratitis, N., Jayasena, S. and Gold, L.
TITLE High affinity nucleic acid ligands of cytokines
JOURNAL Patent: US 5972599-A 37 26-OCT-1999;
FEATURES location/Qualifiers
source 1..70
/organism="unknown"

BASE COUNT 13 a 16 c 31 g 10 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gggcgagcagcgcg 14
1 | | | | | | | | | |
Db 12 GGGGTCGAGCGCGG 25

RESULT 15
MZETAC1 74 bp DNA linear PLN 27-APR-1993
LOCUS MZETAC1
DEFINITION Z.mays transposon Ac insertion sequence 1, allele bz-m2(Ac).

Query Match 100.0%; Score 15; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgcg 15
| | | | | | | | | | | | | | |
DB 1 gcgcgcgcgcgcgcg 15

RESULT 4

AAK18699
ID AAK18699 standard; DNA; 15 BP.

AC AAK18699;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #31.

KW Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KW HIV; inflammation; ss.

OS Synthetic.

PN WO9901579-A1.

PD 14-JAN-1999.

PF 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

PA (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

DR WPI, 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used

PT particularly for delivering therapeutic antisense oligonucleotides

PS across the gastrointestinal mucosa, provides high bioavailability

XX Example 2; Page 86; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a

CC nucleic acid and at least one penetration enhancer. The compositions are

CC used: (1) to treat or prevent any disease or disorder that can be

CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,

CC beta-thalassemia, malaria, viral infections (including human immune

CC deficiency virus (HIV), inflammation, in human or animal medicine;

CC (11) to investigate the role of a gene or gene product in non-human

CC animals; and (11) to modulate gene expression in cells, tissues or

CC organs. The compositions provide bioavailability of at least 15,

CC preferably 17-35%. The penetration enhancer improves: (1) transport of

CC the nucleic acid across the mucosa of the alimentary canal and into

CC cells; and (11) increases stability of the nucleic acid. Oral

CC administration avoids the complications and expense of intravenous or

CC other methods of administration. AAK18699 to AAK18799 and AAK18801

CC represent antisense oligonucleotides which can be used as the nucleic

CC acid in the method of the invention.

XX Sequence 15 BP; 1 A; 5 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgcg 15
| | | | | | | | | | | | | | |
DB 1 gcgcgcgcgcgcgcg 15

RESULT 5

AAF45301/c
ID AAF45301 standard; DNA; 15 BP.

AC AAF45301;

DT 30-MAR-2001 (first entry)

DE IGFBP2 oligonucleotide #140.

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; psoriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000NO-AU00693.

PR 21-JUN-1999; 99US-0140345.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by

PT administering UV (ultra-violet) treatment (optional) and an antisense

PT nucleic acid that inhibits or reduces growth factor mediated cell

PT proliferation and/or inflammation -

PS proliferation and/or inflammation -

XX Example 6; Page 35; 201pp; English.

CC The present invention relates to a method for ameliorating the effects

CC of skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and

CC AAF45153-F45161). The method is useful for ameliorating the effects of

CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,

CC keratosis, neoplasia, scleroderma, warts, benign growths, cancers of the

CC skin, a hyperneovascular condition such as a neovascular condition of the

CC retina, brain or skin, growth factor-mediated malignancies, other

CC sclerotic disease, kidney disease, hyperproliferation of the inside of

CC blood vessels or any other hyperplasia.

XX Sequence 15 BP; 0 A; 8 C; 5 G; 2 T; 0 other;

Query Match 89.3%; Score 13.4; DB 22; Length 15;

Best Local Similarity 93.3%; Pred. No. 3.6e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgcg 15
| | | | | | | | | | | | | | |
DB 15 GCAGCGCGCAGCGCG 1

RESULT 6

AAH49944
ID AAH49944 standard; DNA: 33 BP.
XX
AC AAH49944;
XX
DT 22-AUG-2001 (first entry)
XX
DE Bacterial 23S/5S RNA detecting primer SEQ ID 139.
XX
KM Detection: spacer: 23S rDNA; 5S rDNA; probe: phylogenetic group;
XX enterobacterium; clinical diagnosis; food contamination; ss.
OS Erwinia chrysanthemi.
XX
PN DE19945916-A1.
XX
PD 05-APR-2001.
XX
PF 24-SEP-1999; 99DE-1045916.
XX
PR 24-SEP-1999; 99DE-1045916.
XX
PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI Grabowski R, Berghof K;
XX
DR WPI; 2001-246133/26.
XX
PT New nucleic acid primers and probes, useful for bacterial detection, in
PT clinical diagnosis and detecting food contamination, comprises 23S and
PT 5S rDNA sequences -
XX
PS Claim 17; Page 63; 140pp; German.
XX
CC This invention describes a novel nucleic acid molecule (I), useful as a
CC probe and/or primer for detecting bacteria. The invention also describes
CC (1) a combination of at least two nucleic acids (II) for detecting
CC bacteria or phylogenetic groups of bacteria, particularly enterobacteria;
CC (2) a kit containing (I) or the combination of (II); (3) detecting
CC bacteria (particularly enterobacteria) in a sample by contacting the
CC sample with (I) or the combination of (II) and detecting hybridization;
CC and (4) amplifying (MI) bacterial DNA from many different taxonomic
CC groups using (I) or the combination of (II) as primers. The method is
CC used to detect and identify bacteria, for clinical diagnosis and for
CC detecting contamination of food. (I) can detect bacteria at various
CC levels of selectivity (e.g., all bacteria, particular classes, families,
CC genera or species). The method exploits the fact that the 23S and 5S rDNA
CC regions, and the intermediate transcribed spacer, contain some sequences
CC that are highly conserved and others that are highly variable.
CC AAH49807-AAH50411 represent primers used to illustrate the method of the
CC invention.
XX
SQ Sequence 33 BP; 3 A; 11 C; 14 G; 5 T; 0 other;

Query Match 89.3%; Score 13.4; DB 22; Length 33;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
|||||
Db 6 ggcggcgtagcgcg 20

RESULT 7
AAF81441/C
ID AAF81441 standard; DNA: 40 BP.
XX
AC AAF81441;
XX
DT 08-JUN-2001 (first entry)
XX
DE PCR primer GSP2 for corn promoter clone #700164205.

XX
KM Corn; promoter; transgenic plant; herbicide resistance; PCR primer; ss.
XX
OS Zea mays.
XX
PN WO200119976-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US25078.
XX
PR 16-SEP-1999; 99US-0154182.
XX
PA (MONS) MONSANTO CO.
XX
PI Anderson HM, Chay CA, Chen G, Conner TW;
XX
DR WPI; 2001-244796/25.
XX
PT Novel promoter nucleic acid sequences useful for regulating
PT heterologous gene expression in plants, comprising regulatory sequences
PT located upstream to plant DNA structural coding sequences -
XX
PS Example 3; Page 87; 101pp; English.
XX
CC The present invention relates to novel corn promoter sequences (see
CC AAF81456-AAF81478). The promoter sequences are useful for conferring
CC expression of a second polynucleotide molecule in a transgenic plant
CC tissue. In addition, the promoter sequences are useful for providing
CC plants with herbicide resistance. The promoter sequences are suitable for
CC selectively modulating expression of any operatively linked gene and
CC provide additional regulatory element diversity in a plant expression
CC vector in gene stacking approaches. The present sequence is a PCR primer
CC used in the present invention.
XX
SQ Sequence 40 BP; 3 A; 17 C; 13 G; 7 T; 0 other;

Query Match 89.3%; Score 13.4; DB 22; Length 40;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
|||||
Db 26 GCGGCGCGCACGCGG 12

RESULT 8
AAL29213
ID AAL29213 standard; DNA: 51 BP.
XX
AC AAL29213;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2421.
XX
KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KM amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinesin; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
DE 28-DEC-2000; 2000WO-US35498.

PA (AFY-) AFFYMETRIX INC.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 PI Fan JB, Chakravarti A, Haluska MK;
 XX
 DR WPI; 2000-107928/10.
 XX
 PT Novel nucleic acids containing polymorphisms used in the diagnosis of
 PT hypertension -
 XX
 PS Claim 1; Page 16; 53pp; English.
 CC The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC Insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Miskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals.
 XX
 SQ Sequence 29 BP; 4 A; 11 C; 6 G; 7 T; 1 other;

Query Match 86.7%; Score 13; DB 21; Length 29;
 Best Local Similarity 86.7%; Pred. No. 5e+03;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 gcggcgagcgagcg 15
 ||||| ||||| |||||
 Db 26 GCGGAGCGACGCCG 12

RESULT 11
 AAF45300/C
 ID AAF45300 standard; DNA; 15 BP.

AC AAF45300;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #139.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU00693.
 XX
 PR 21-JUN-1999; 99US-0140345.
 XX

PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX
 PS Example 6; Page 35; 201pp; English.
 CC The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX
 SQ Sequence 15 BP; 0 A; 8 C; 5 G; 2 T; 0 other;

Query Match 82.7%; Score 12.4; DB 22; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 cgagcgagcgagcg 15
 | ||||| |||||
 Db 15 CAGCGGACGCCGCG 2

RESULT 12
 AAF45302/C
 ID AAF45302 standard; DNA; 15 BP.

AC AAF45302;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #141.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU00693.
 XX
 PR 21-JUN-1999; 99US-0140345.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;

PT DNA encoding the Helicoverpa armigera granulovirus enhancer protein

The present invention relates to antisense compounds up to 30 nucleobases in length targeted to a E2F transcription factor 1. The invention is useful for inhibiting the expression of E2F transcription factor 1 in cells or tissues. The antisense oligonucleotides may also be used as a research agent and to prevent infection, inflammation or tumours.

Query Match	82.7%	Score 12.4;	DB 22;	Length 20;
Best Local Similarity	92.9%;	Pred. No. 9.4e+03;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcgcgcgcgcgcgcg 15
|||||
Db 1 ggcgcgcgcgcgcgcg 15

RESULT 2
US-09-080-285-14
; Sequence 14, Application US/09080285
; Patent No. 6040181

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

US-09-080-285-14

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcgcgcgcgcgcgcg 15
|||||
Db 1 ggcgcgcgcgcgcgcg 15

RESULT 3
US-08-465-485A-28
; Sequence 28, Application US/08465485A
; Patent No. 5831066

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:

NAME/KEY: Modified_base

LOCATION: 18..19

OTHER INFORMATION: Last two internucleoside linkages are

US-08-465-485A-28

Query Match 86.7%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcgcgcgcgcgcgcg 13
|||||
Db 8 ggcgcgcgcgcgcgcg 20

RESULT 4
US-09-080-285-28
; Sequence 28, Application US/09080285
; Patent No. 6040181

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphothioates
US-09-080-285-28

Query Match 86.7%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcgagcagcg 13
|||||
DB 8 gcggcgagcagcg 20

RESULT 5
US-09-517-584A-13
Sequence 13, Application US/09517584A
Patent No. 6187587
GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Vickie L. Brown-Driver

APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 1 EXPRES
FILE REFERENCE: RTS-0121
CURRENT APPLICATION NUMBER: US/09/517,584A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-13

Query Match 82.7%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcggcgagcagcg 14
|||||
DB 7 gcggcgagcagcg 20

RESULT 6
US-08-477-527A-37
Sequence 37, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClellan
REGISTRATION NUMBER: 34,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-046-894-28

Query Match 80.0%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgc 12
|||||
Db 2 GCGGCGGCGCGC 13

RESULT 12
US-09-914-961-2/c
Sequence 2, Application US/08914961
Patent No. 6018042

GENERAL INFORMATION:

APPLICANT: Mett, Helmut
APPLICANT: Haner, Robert
APPLICANT: Dean, Nicholas Mark
TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Editor

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/914,961
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/287,753
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spivill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4-20047/P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8615
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

POSITION IN GENOME:
MAP POSITION: -80
UNITS: bp
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..20
OTHER INFORMATION: /note="All nucleotides are of the
phosphorothioate type"
US-08-914-961-2

Query Match 80.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgc 12
|||||
Db 17 GCGGCGGCGCGC 6

RESULT 13

US-08-651-136C-43
Sequence 43, Application US/08651136C
Patent No. 6001639

GENERAL INFORMATION:

APPLICANT: Schuelein, Martin
APPLICANT: Andersen, Iene N.
APPLICANT: Lassen, Soren F.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Lange, Iene
APPLICANT: Nielsen, Rudy I.

APPLICANT: Ihara, Michiko

APPLICANT: Takagi, Shinobu

TITLE OF INVENTION: No. 6001639e1 Endoglucanases

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 60016390 No. 6001639d1 of No. 6001639th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..63
US-08-651-136C-43

Query Match 80.0%; Score 12; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

	Matches	12: Conservative	0: Mismatches	0: Indels	0: Gaps
QY	2	CGGCGGCGAGGC	13		
Db	9	CGGCGGCGAGGC	20		

RESULT 14
 US-08-318-193-32
 ; Sequence 32, Application US/08318193
 ; Patent No. 5641663
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: GARVIN, Robert T.
 ;
 ; APPLICANT: MALEK, Lawrence T.
 ;
 ; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
 ;
 ; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
 ;
 ; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
 ;
 ; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
 ;
 ; NUMBER OF SEQUENCES: 91
 ;
 ; CORRESPONDENCE ADDRESS:

```

1 ADDRESSSEE: Foley & Lerner
2 STREET: 1800 Diagonal Road, Suite 500
3 CITY: Alexandria
4 STATE: Virginia
5 COUNTRY: USA
6 ZIP: 22313-0299
7
8 COMPUTER READABLE FORM:
9
10 MEDIUM TYPE: Floppy disk
11 OPERATING SYSTEM: IBM PC compatible
12 SOFTWARE: Patentin Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/318,193
15 FILING DATE:
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US/07/935,314
19 FILING DATE:
20 APPLICATION NUMBER: US 07/224,568
21 ATTORNEY/AGENT INFORMATION:
22 NAME: BENT, Stephen A.
23 REGISTRATION NUMBER: 29,768
24 REFERENCE/DOCKET NUMBER: 18740/116 CACO
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (703)836-9300
27 TELEFAX: (703)663-4109
28 TELEX: 889149
29
30 INFORMATION FOR SEQ ID NO: 32:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 73 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: other nucleic acid;
37 DESCRIPTION: Synthetic DNA oligonucleotide
38 ANTI-SENSE: YES
39
40 US-08-318-193-32

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Query Match 80.0%; Score 12; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcgcgcgcacgc 12
Db 37 GCGCGCGCAGCG 48

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RESULT 15
US-09-593-323-34
; Sequence 34, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:

```

? APPLICANT: Morgan, Antony R.
? APPLICANT: Severini, Alberto
? TITLE OF INVENTION: Compositions and Methods for Determining the Activity
? TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
? TITLE OF INVENTION: Transcription
? FILE REFERENCE: DNAB-02921
? CURRENT APPLICATION NUMBER: US/09/5993,323
? CURRENT FILING DATE: 2000-06-13
? PRIOR APPLICATION NUMBER: 09/344,300
? PRIOR FILING DATE: 1999-06-24
? NUMBER OF SEQ. ID NOS: 72
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 34
? LENGTH: 18
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? US-09-593-323-34

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		78.7%;	Score 11.8;	DB 4;	Length 18;
Query Match		86.7%;	Pred. No. 5.3e+03;		
Best Local Similarity					
Matches 13; Conservative		0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1 ggcggcgagcgcg	15			
Db	1 ggcggcgagcgcg	15			

Search completed: June 28, 2002, 22:16:51
Job time: 8277 sec

Mon Jul 1 08:40:49 2002

us-09-709-170a-14.szlm75.rni

Query Match	100.0%;	Score 15;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	1.1e+04;	

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
|||||
Db 1 CGCGCGGCGCACGGA 15

RESULT 2

A36502 69 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 43 from Patent WO9323549.
DEFINITION A36502
ACCESSION A36502.1 GI:2293813
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Aurias,A., Delattre,O., Desmaze,C., Melot,F., Peter,M.,
1 (bases 1 to 69)
TITLE NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED IN
RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE
DEVELOPMENT OF CANCEROUS TUMORS
JOURNAL Patent: WO 9323549-A 43 25-NOV-1993;
COMMENT CENTRE NAT RECH SCIENT (FR)
Other publication FR 2691475 931126
Other publication JP 85009647 960206.

FEATURES
source 1..69
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 15 a 17 c 28 g 9 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 69;
Best Local Similarity 93.3%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
|||||
Db 45 CGCGCGGCGCACGGA 59

RESULT 3
LOCUS AR080135 69 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 46 from patent US 5968734.
ACCESSION AR080135
VERSION AR080135.1 GI:10006870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 69)
AUTHORS Aurias,A., Delattre,O., Desmaze,C., Melot,F., Peter,M.,
TITLE Nucleic acid corresponding to a gene of chromosome 22 involved in
recurrent chromosomal translocations associated with the
development of cancerous tumors, and nucleic acids of fusion
resulting from said translocations
JOURNAL Patent: US 5968734-A 46 19-OCT-1999;
FEATURES location/Qualifiers
source 1..69
/organism="unknown"
BASE COUNT 15 a 17 c 28 g 9 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 69;
Best Local Similarity 93.3%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
|||||
Db 45 CGCGCGGCGCACGGA 59

RESULT 4

EPKRRN04 21 bp RNA linear PLN 13-APR-1994
LOCUS Ephedra tweediana 28S ribosomal RNA (28S rRNA), ca. bp 2019 to 2039
DEFINITION in mature RNA.
ACCESSION M82019
VERSION M82019.1 GI:471000
KEYWORDS 28S ribosomal RNA.
SEGMENT 4 of 5
SOURCE Ephedra tweediana RNA.
ORGANISM Ephedra tweediana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnepophyta; Gnepopsida; Ephedrales; Ephedraceae;
Ephedra.

REFERENCE
AUTHORS Hamby,R.K., Sub.Y.B., Bult,C.J., Kallersjo,M. and Zimmer,E.A.
1 (bases 1 to 21)
TITLE Darwin's abominable mystery revisited: Ribosomal RNA insights into
flowering plant evolution
JOURNAL Unpublished (1991)
REFERENCE 2 (sites)
AUTHORS Doyle,J.A., Donoghue,M.J. and Zimmer,E.A.
TITLE Integration of morphological and ribosomal RNA data on the origin
of angiosperms
JOURNAL Ann. Missouri Bot. Garden (1994) In press
FEATURES location/Qualifiers
source 1..21
/organism="Ephedra tweediana"
/db_xref="taxon:3390"

BASE COUNT 1 a 7 c 11 g 2 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 8; Length 21;
Best Local Similarity 92.9%; Pred. No. 1.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 14
|||||
Db 8 CGCGTGGCGACGCG 21

RESULT 5
EPKRRN04 21 bp RNA linear PLN 15-JUN-1994
LOCUS Ephedra distachya 28S ribosomal RNA (28S rRNA), ca. bp 2019 to 2039
DEFINITION in mature RNA.
ACCESSION M82279
VERSION M82279.1 GI:471006
KEYWORDS 28S ribosomal RNA.
SEGMENT 4 of 5
SOURCE Ephedra distachya RNA.
ORGANISM Ephedra distachya
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnepophyta; Gnepopsida; Ephedrales; Ephedraceae;
Ephedra.

REFERENCE
AUTHORS Hamby,R.K., Sub.Y.B., Bult,C.J., Kallersjo,M. and Zimmer,E.A.
1 (bases 1 to 21)
TITLE Darwin's abominable mystery revisited: Ribosomal RNA insights into
flowering plant evolution
JOURNAL Unpublished (1991)
REFERENCE 2 (sites)
AUTHORS Doyle,J.A., Donoghue,M.J. and Zimmer,E.A.
TITLE Integration of morphological and ribosomal RNA data on the origin
of angiosperms
JOURNAL Ann. Missouri Bot. Garden (1994) In press
FEATURES location/Qualifiers
source 1..21

LOCUS S86495 24 bp mRNA linear ROD 16-APR-2001
 DEFINITION Rattus norvegicus T cell receptor beta chain variable (TCR Vbeta6/Jbeta2.3) mRNA, partial cds.
 ACCESSION S86495
 VERSION S86495.1 GI:247004
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 24)
 Gold, D.P., Vainiene, M., Celtnik, B., Wiley, S., Gibbs, C., Hashim, G.A., Vandenbark, A.A. and Offner, H. Characterization of the immune response to a secondary encephalitogenic epitope of basic protein in Lewis rats. II. Biased T cell receptor V beta expression predominates in spinal cord infiltrating T cells
 J. Immunol. 148 (6), 1712-1717 (1992)
 JOURNAL 92176627
 MEDLINE 1371786
 PUBMED
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gidsq 86495] from the original journal article.
 This sequence comes from Table IV.
 FEATURES
 SOURCE location/Qualifiers
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 /strain="Lewis"
 /db_xref="taxon:10116"
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 /gene="TCR Vbeta6/Jbeta2.3"
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cggcgggcgagcaga 15
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 Db 6 CGGGGGCGGCGAGCA 20
 RESULT 11
 AX116381 51 bp DNA linear PAT 11-MAY-2001
 LOCUS AX116381
 DEFINITION Sequence 1504 from Patent WO0129262.
 ACCESSION AX116381
 VERSION AX116381.1 GI:14033323
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 51)
 Picoult-Newburg, L. and Pohl, M. Genotyping reagents, kits and methods of use thereof
 Patent: WO 0129262-A 1504 26-APR-2001;
 JOURNAL Orchid Biosciences, Inc. (US)
 TITLE location/Qualifiers
 1..51
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 8 a 25 c 5 g 13 t
 ORIGIN
 Query Match 78.7%; Score 11.8; DB 6; Length 51;
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 cggcgggcgagcaga 15
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 Db 20 CGGGGGCGGAGGGA 6
 RESULT 12
 AR159674/c 52 bp DNA linear PAT 17-OCT-2001
 LOCUS AR159674/c
 DEFINITION Sequence 14 from patent US 6251606.
 ACCESSION AR159674
 VERSION AR159674.1 GI:16222414
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 52)
 Hseu, R. and Chen, C. Gene sequence and method for distinguishing cordyceps sinensis
 Patent: US 6251606-A 14 26-JUN-2001;
 JOURNAL location/Qualifiers
 FEATURES source
 1..52
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 ORIGIN
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 Db 29 CGGGGGCGGCGCGGA 15
 RESULT 13
 HSTCP22B 57 bp mRNA linear PRI 18-JUL-1997
 LOCUS HSTCP22B
 DEFINITION H.sapiens mRNA for T cell receptor beta chain region (TCRBV21S4BJ2S3).
 ACCESSION Z49925
 VERSION Z49925.1 GI:887474
 KEYWORDS T cell receptor; T cell receptor beta chain.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 57)
 Silins, S.L. Direct Submision
 Submitted (23-JUN-1995) Silins S. L., Queensland Institute of Medical Research, EBV unit, The Pancoft Centre, 300 Herston Road, Brisbane, Queensland, AUSTRALIA, 4029
 2 (bases 1 to 57)
 Burrows, S.R., Silins, S.L., Moss, D.J., Khanna, R., Misko, I.S. and Argat, V.P. T cell receptor repertoire for a viral epitope in humans is diversified by tolerance to a background major histocompatibility complex antigen
 The Journal of experimental medicine. 182 (6), 1703-1715 (1995)
 JOURNAL 96096444
 MEDLINE 7500015
 PUBMED
 REFERENCE 3 (bases 1 to 57)
 Burrows, S.R., Silins, S.L., Moss, D.J., Khanna, R., Misko, I.S. and Argat, V.P.

TITLE T cell receptor repertoire for a viral epitope in humans is
JOURNAL J. Exp. Med. 182, 1-13 (1995)
FEATURES
SOURCE Location/Qualifiers
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/tissue_type="blood"
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/db_xref="GI:887475"
/translation="CASFSWTSWGATDQYFG"
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Best Local Similarity 86.7%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcgggcgacgga 15
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Db 27 CGGGGGGGCGACAGA 41

RESULT 14
LOCUS HSU91293 69 bp mRNA linear PRI 03-JUL-1997.
DEFINITION Homo sapiens T-cell receptor delta chain (TCRDV3J1) mRNA, partial cds.
ACCESSION U91293
VERSION U91293.1 GI:2239991
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 69)
Holtmeier, W., Wiltthoft, T., Hennemann, A., Wlnter, H.S. and Kagnoff, M.F.
The TCR-delta repertoire in human intestine undergoes characteristic changes during fetal to adult development
J. Immunol. 158 (12), 5632-5641 (1997)
2 (bases 1 to 69)
Holtmeier, W., Wiltthoft, T., Hennemann, A., Harland, S.W. and Kagnoff, M.F.
Direct Submission
Submitted (27-FEB-1997) Department of Medicine, University of Frankfurt, Theodor-Stein Kai #7, Frankfurt 60590, Germany
JOURNAL
TITLE Location/Qualifiers
1..69
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J. Exp. Med. 179:323-328, 1994"
/product="T-cell receptor delta chain"
/protein_id="AAC51509.1"
/db_xref="GI:2239992"
/translation="TEDSATYTCAFKSVKAGATDKLT"
BASE COUNT 17 a 21 c 16 g 15 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 9; Length 69;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcgggcgacgga 15
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Db 45 CGCCGGGGCGACCGA 59

RESULT 15
LOCUS DUCRRN04 21 bp RNA linear PLN 13-APR-1994
DEFINITION Duchesnea indica 28S ribosomal RNA (28S RNA), ca. bp 2019 to 2039 in mature RNA.
ACCESSION M82284
VERSION M82284.1 GI:470940
KEYWORDS 28S ribosomal RNA.
SEGMENT 4 of 5
SOURCE Duchesnea indica RNA.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Duchesnea.
REFERENCE 1 (bases 1 to 21)
Hamby, R.K., Suh, Y.B., Bult, C.J., Kallersjo, M. and Zimmer, E.A.
Darwin's abominable mystery revisited: Ribosomal RNA insights into flowering plant evolution
unpublished (1991)
2 (sites)
Doyle, J.A., Donoghue, M.J. and Zimmer, E.A.
Integration of morphological and ribosomal RNA data on the origin of angiosperms
Ann. Missouri Bot. Garden (1994) In press
JOURNAL
TITLE Location/Qualifiers
1..21
/organism="Duchesnea indica"
/db_xref="taxon:13044"

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
1..21
/organism="Duchesnea indica"
/db_xref="taxon:13044"

BASE COUNT 1 a 6 c 10 g 1 t 3 others
ORIGIN

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Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 8 CGCCGGGGCGACCG 21

Search completed: June 28, 2002, 22:11:17
Job time: 8368 sec

Mon Jul 1 08:40:50 2002

us-09-709-170a-15.szlm75.rge

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:18 ; Search time 3762.88 Seconds
(without alignments)
100.104 Million cell updates/sec

Title: US-09-709-170a-17

Perfect score: 18
Sequence: 1 tctccagcgtgcgcacat 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: gb_ba:*
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33: em_hlg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	18	100.0	18	AR052619	Sequence
2	18	100.0	18	AR052624	Sequence
3	18	100.0	18	ARI16926	Sequence
4	18	100.0	18	ARI40496	Sequence
5	18	100.0	18	ARI46347	Sequence
6	18	100.0	18	ARI46392	Sequence
7	18	100.0	18	ARI54716	Sequence
8	18	100.0	18	ARI67448	Sequence
9	18	100.0	18	AX015198	Sequence
10	18	100.0	18	AX020948	Sequence
11	18	100.0	18	AX020954	Sequence
12	18	100.0	18	AX020959	Sequence
13	18	100.0	18	AX040169	Sequence
14	18	100.0	18	AX040403	Sequence
15	18	100.0	18	AX063576	Sequence
16	18	100.0	18	AX081353	Sequence
17	18	100.0	18	AX083693	Sequence
18	18	100.0	18	AX088930	Sequence
19	18	100.0	18	AX103809	Sequence
20	18	100.0	18	AX103862	Sequence
21	18	100.0	18	AX103863	Sequence
22	18	100.0	18	AX103899	Sequence
23	18	100.0	18	AX105211	Sequence
24	18	100.0	18	AX135635	Sequence
25	18	100.0	18	AX283183	Sequence
26	18	100.0	18	AX283250	Sequence
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36	18	100.0	27	AX083688	Sequence
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38	18	100.0	27	143661	Sequence
39	18	100.0	27	186720	Sequence
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LOCUS	AR052619				
DEFINITION	Sequence 17 from patent US 5831066.				
ACCESSION	AR052619				
VERSION	AR052619.1	GI:5975963			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	Reed,J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 17 03-NOV-1998;				
FEATURES	Location/Qualifiers				
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Db 1 TCTCCAGCGTGCACAT 18

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AR052624 AR052624 18 bp DNA 11near PAT 29-SEP-1999

LOCUS AR052624 Sequence 24 from patent US 5831066.
ACCESSION AR052624
VERSION AR052624.1 GI:5975988

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Reed,J.C.

TITLE Regulation of bcl-2 gene expression

JOURNAL Patent: US 5831066-A 24 03-NOV-1998;

FEATURES Location/Qualifiers

source

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 3

LOCUS AR116926 AR116926 18 bp DNA 11near PAT 16-MAY-2001

DEFINITION Sequence 1 from patent US 6140051.

ACCESSION AR116926

VERSION AR116926.1 GI:14097832

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Brown,L.R. and Xu,C.

TITLE Fluorescent dibenzazole derivatives and methods related thereto

JOURNAL Patent: US 6140051-A 1 31-OCT-2000;

FEATURES Location/Qualifiers

source

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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RESULT 4

LOCUS AR140496 AR140496 18 bp DNA 11near PAT 16-JUN-2001

DEFINITION Sequence 55 from patent US 6207646.

ACCESSION AR140496

VERSION AR140496.1 GI:14482992

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M., Kline,J., Kliman,D. and Steinberg,A.D.

TITLE Immunostimulatory nucleic acid molecules

JOURNAL Patent: US 6207646-A 55 27-MAR-2001;

FEATURES Location/Qualifiers

source

BASE COUNT 2 a 8 c 4 g 4 t

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Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 5

LOCUS AR146347 AR146347 18 bp DNA 11near PAT 08-AUG-2001

DEFINITION Sequence 59 from patent US 6218371.

ACCESSION AR146347

VERSION AR146347.1 GI:15109536

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M. and Weiner,G.

TITLE Methods and products for stimulating the immune system using

JOURNAL immunotherapeutic oligonucleotides and cytokines

Patent: US 6218371-A 59 17-APR-2001;

FEATURES Location/Qualifiers

source

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCTCCAGCGTGCACAT 18

RESULT 6

LOCUS AR146392 AR146392 18 bp DNA 11near PAT 08-AUG-2001

DEFINITION Sequence 104 from patent US 6218371.

ACCESSION AR146392

VERSION AR146392.1 GI:15109581

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M. and Weiner,G.

TITLE Methods and products for stimulating the immune system using

JOURNAL immunotherapeutic oligonucleotides and cytokines

Patent: US 6218371-A 104 17-APR-2001;

FEATURES Location/Qualifiers

source

BASE COUNT 2 a 8 c 4 g 4 t

ORIGIN

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Db 1 TCTCCAGCGTGC GCCAT 18

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LOCUS AR154716 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 45 from patent US 6239116.
ACCESSION AR154716
VERSION AR154716.1 GI:15122769
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg, A.M. and Kline, J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 45 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..18

BASE COUNT 2 a 8 c 4 g 4 t
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Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCTCCAGCGTGC GCCAT 18

RESULT 8
LOCUS AR167448 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 14 from patent US 6287591.
ACCESSION AR167448
VERSION AR167448.1 GI:17903228
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Semple, S.C., Klimuk, S.K., Harasym, T., Hope, M.J., Ansell, S.M.,
Cullis, P., Scherrer, P. and Debever, D.
TITLE Charged therapeutic agents encapsulated in lipid particles
JOURNAL Patent: US 6287591-A 14 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..18

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGC GCCAT 18

RESULT 9
LOCUS AX015198 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9952549.
ACCESSION AX015198
VERSION AX015198.1 GI:10041241
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friede, M. and Hermand, P.
TITLE Adjuvant compositions
JOURNAL Patent: WO 9952549-A 2 21-OCT-1999;
SMITHKLINE BEECHAM BIOLOG (BE); FRIEDE MARTIN (BE); HERMAND
PHILIPPE (BE)

FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGC GCCAT 18

RESULT 10
LOCUS AX020948 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 25 from Patent WO933868.
ACCESSION AX020948
VERSION AX020948.1 GI:10044612
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Dalemans, W.L. and Gerard, C.M.
TITLE Vaccine
JOURNAL Patent: WO 9933868-A 25 08-JUL-1999;
DALEMANS WILFRIED L J (BE); SMITHKLINE BEECHAM BIOLOG (BE); GERRARD
CATHERINE MARIE GHISLAI (BE)

FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGC GCCAT 18

RESULT 11
LOCUS AX020954 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from Patent WO933488.

ACCESSION AX020954
 VERSION AX020954.1 GI:10044617
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

AX020954
 AX020954.1 GI:10044617
 synthetic construct.
 synthetic construct.
 artificial sequence.
 1 (bases 1 to 18)
 Dalemans, W.L., Priels, J.P. and Lafertiere, C.A.
 Vaccine
 Patent: WO 9933488-A 4 08-JUL-1999;
 DALEMANNS WILFRIED L.J (BE); PRIELS JEAN PAUL (BE); SMITHKLINE
 BEECHAM BIOLOG (BE); LAFERIERE CRAIG ANTONY JOSEPH (BE)

FEATURES
 source
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 /organism="synthetic construct"
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 /note="this is a synthetic oligonucleotide"

BASE COUNT 2 a 8 c 4 g 4 t
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QY 1 tctccagcgtgcgcacat 18
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 Db 1 TCTCCACGCGTGCACCAT 18

RESULT 12
 AX040169 18 bp DNA linear PAT 18-NOV-2000
 LOCUS
 DEFINITION Sequence 2 from Patent WO0062800.
 ACCESSION AX040169
 VERSION AX040169.1 GI:11230119
 KEYWORDS
 SOURCE
 ORGANISM

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (bases 1 to 18)
 Friede, M., Garcon, N. and Hermand, P.
 Adjuvant composition comprising saponin and an immunostimulatory o
 ligonucleotide
 Patent: WO 0062800-A 2 26-OCT-2000;
 SmithKline Beecham Biologicals s.a. (BE)

FEATURES
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 1..18
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2 a 8 c 4 g 4 t
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QY 1 tctccagcgtgcgcacat 18
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RESULT 13
 AX040403 18 bp DNA linear PAT 18-NOV-2000
 LOCUS
 DEFINITION Sequence 2 from Patent WO0062802.
 ACCESSION AX040403
 VERSION AX040403.1 GI:11230215
 KEYWORDS
 SOURCE
 ORGANISM

artificial sequence.
 1 (bases 1 to 18)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (bases 1 to 18)
 Deschamps, M.
 Vaccine comprising rsv antigen and cpg oligonucleotide
 Patent: WO 0062802-A 2 26-OCT-2000;
 SmithKline Beecham Biologicals s.a. (BE)

FEATURES
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 /organism="synthetic construct"
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RESULT 14
 AX063576 18 bp DNA linear PAT 24-JAN-2001
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 DEFINITION Sequence 2 from Patent WO0100231.
 ACCESSION AX063576
 VERSION AX063576.1 GI:12541300
 KEYWORDS
 SOURCE
 ORGANISM

synthetic construct.
 synthetic construct
 artificial sequence.
 1 (bases 1 to 18)
 Cohen, J., Garcon, N. and Voss, G.
 Vaccines
 Patent: WO 0100231-A 2 04-JAN-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES
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RESULT 15
 AX081353 18 bp DNA linear PAT 27-FEB-2001
 LOCUS
 DEFINITION Sequence 32 from Patent WO0108707.
 ACCESSION AX081353
 VERSION AX081353.1 GI:13170195
 KEYWORDS
 SOURCE
 ORGANISM

synthetic construct.
 synthetic construct
 artificial sequence.
 1 (bases 1 to 18)
 Uhlmann, E., Greiner, B., Unger, E., Gothe, G. and Schwerdel, M.
 Conjugates and methods for the production thereof, and their use
 for transporting molecules via biological membranes
 Patent: WO 0108707-A 32 08-FEB-2001;
 Aventis Pharma Deutschland GmbH (DE)

FEATURES

Location/Qualifiers

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/note="Oligonucleotide"
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Job time: 8370 sec

